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NUCLEIC ACIDS ENCODING ION CHANNELS

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Nucleic acids encoding ion channels, and methods of using same, are disclosed.

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(54) Title: NUCLEIC ACIDS ENCODING ION CHANNELS

(57) Abstract: Nucleic acids encoding ion channels, and methods of using same, are disclosed.

NUCLEIC ACIDS ENCODING ION CHANNELS

RELATED APPLICATIONS

This application is a continuation-in-part application of and claims priority to U.S Provisional Application 60/302,082, filed June 29, 2001 and to U.S. Provisional Application 60/332,835, filed November 6, 2001, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

An ion channel is a protein-lined pore in a membrane that provides an aqueous environment through which ions can cross the hydrophobic lipid bilayer. Ion channels are specific for anions or cations and many are specific for one type or a small set of ions. Some ion channels are permanently open allowing passive transport of ions down their electrochemical gradients. Most however are gated and open only in response to a stimulus.

The two main types of gated ion channels are the ligand-gated channels, which open in response to binding of a ligand such as a neurotransmitter to a receptor (*e.g.*, excitatory amino acid receptors, GABA and glycine receptors and nicotinic receptors) and voltage-gated ion channels whose opening is controlled by changes of the membrane potential. Upon receptor activation of ligand-gated ion channels, the channel is opened allowing the passage of ions that can, depending on the receptor type, depolarize or hyperpolarize the cell membrane.

Ion channels are involved in an enormous range of biological processes for cell to cell signaling and are essential for interaction between cells and with the environment.

SUMMARY OF THE INVENTION

The present invention relates to ion channel genes, particularly nucleic acids comprising ion channel genes, and the amino acids encoded by such nucleic acids. These sequences are shown in Table I. In Table I, each ion channel entry lists the name (*e.g.*, "MOOSE03990"), the University of California at Santa Cruz contig designation from which the sequence was analyzed (*e.g.*, "ctg17115"), the exon locations (*e.g.*, "505609..505687, 505992, . . ."), following by the amino acid sequence and the nucleic acid sequence.

Sub-family information on the sequences is shown in Table II. For each sequence, the following information is provided: the University of California at Santa Cruz contig designation from which the sequence was analyzed (*e.g.*, "ctg17115"), the name (*e.g.*, "MOOSE03990"), and the subfamily to which the sequence appears to belong. The assignments were made on the basis of the best E-value with which the sequence aligned.

In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7 and 9, as shown in Table I, and the complements thereof. The invention further relates to a nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7 and 9, as shown in Table I, and the complements thereof. The invention additionally relates to isolated nucleic acid molecules (*e.g.*, cDNA molecules) encoding an ion channel polypeptide (*e.g.*, encoding a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, 6, 8 and 10, as shown in Table I).

The invention further provides a method for assaying a sample for the presence of a nucleic acid molecule comprising all or a portion of an ion channel in a sample, comprising contacting said sample with a second nucleic acid molecule comprising a nucleotide sequence encoding an ion channel polypeptide (*e.g.*, one of SEQ ID NOs:1, 3, 5, 7 and 9, as shown in Table I, or the complement of one of SEQ ID NOs:1, 3, 5, 7 and 9; a nucleotide sequence encoding one of SEQ ID NOs: 2, 4, 6, 8 and 10, as shown in Table I), or a fragment or derivative thereof, under conditions appropriate for selective hybridization. The invention additionally provides a method for assaying a sample for the level of expression of an ion channel polypeptide, or fragment or derivative thereof, comprising detecting (directly or indirectly) the level of expression of the ion channel polypeptide, fragment or derivative thereof.

The invention also relates to a vector comprising an isolated nucleic acid molecule of the invention operatively linked to a regulatory sequence, as well as to a recombinant host cell comprising the vector. The invention also provides a method for preparing a polypeptide encoded by an isolated nucleic acid molecule described herein (an ion channel polypeptide), comprising culturing a recombinant host cell of the invention under conditions suitable for expression of said nucleic acid molecule.

The invention further provides an isolated polypeptide encoded by isolated nucleic acid molecules of the invention (*e.g.*, ion channel polypeptide), as well as fragments or derivatives thereof. In a particular embodiment, the polypeptide

comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8 and 10, as shown in Table I. The invention also relates to an isolated polypeptide comprising an amino acid sequence which is greater than about 90 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8 and 10, preferably about 95, 96, 97, 98, or 99 percent identical.

The invention also relates to an antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of the invention, as well as to a method for assaying the presence of a polypeptide encoded by an isolated nucleic acid molecule of the invention in a sample, comprising contacting said sample with an antibody which specifically binds to the encoded polypeptide.

The invention further relates to methods of diagnosing a predisposition to a condition mediated by an ion channel. The methods of diagnosing such a predisposition in an individual include detecting the presence of a mutation in an ion channel, as well as detecting alterations in expression of an ion channel polypeptide, such as the presence of different splicing variants of ion channel polypeptides. The alterations in expression can be quantitative, qualitative, or both quantitative and qualitative.

The invention additionally relates to an assay for identifying agents that alter (*e.g.*, enhance or inhibit) the activity or expression of one or more ion channel polypeptides. For example, a cell, cellular fraction, or solution containing an ion channel polypeptide or a fragment or derivative thereof, can be contacted with an agent to be tested, and the level of ion channel polypeptide expression or activity can be assessed. The activity or expression of more than one ion channel polypeptide can be assessed concurrently (*e.g.*, the cell, cellular fraction, or solution can contain more than one type of ion channel polypeptide, such as different splicing variants, and the levels of the different polypeptides or splicing variants can be assessed).

In another embodiment, the invention relates to assays to identify polypeptides that interact with one or more ion channel polypeptides. In a yeast two-hybrid system, for example, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also an ion channel polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the ion channel polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, an ion channel polypeptide binding agent or receptor). Incubation of yeast containing both the first vector and

the second vector under appropriate conditions allows identification of polypeptides which interact with the ion channel polypeptide or fragment or derivative thereof, and thus can be agents which alter the activity of expression of an ion channel polypeptide.

Agents that enhance or inhibit ion channel polypeptide expression or activity are also included in the current invention, as are methods of altering (enhancing or inhibiting) ion channel polypeptide expression or activity by contacting a cell containing ion channel and/or polypeptide, or by contacting the ion channel polypeptide, with an agent that enhances or inhibits expression or activity of ion channel or polypeptide.

Additionally, the invention pertains to pharmaceutical compositions comprising the nucleic acids of the invention, the polypeptides of the invention, and/or the agents that alter activity of ion channel polypeptide. The invention further pertains to methods of treating conditions mediated by ion channel, by administering ion channel therapeutic agents, such as nucleic acids of the invention, polypeptides of the invention, the agents that alter activity of ion channel polypeptide, or compositions comprising the nucleic acids, polypeptides, and/or the agents that alter activity of ion channel polypeptide.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to nucleic acids comprising ion channels, and the ion channel amino acids encoded by those nucleic acids.

Ion channels are involved in regulation of cellular functions, and activation or deactivation of cellular processes, and many of the cellular processes in response to intracellular signals.

Nicotinic acetylcholine receptors, members of the ligand-gated ion channel superfamily, bind to acetylcholine and within milliseconds open a cation channel which permits entry of Na+ and K+ into ther recipient cells, leading to depolarizaton. These receptors are found predominantly in the central nervous system.

Gamma-aminobutyric acid (GABA) receptors that predominate in the brain are the physiological sites of action of the benzodiazepine minor tranquillizers and of barbiturates. These receptors are presumed to be a pentamer with five different classes of subunits each with four membrane spanning regions.

Glutamate/N-methyl-d-aspartate (NMDA) receptor is another class of receptors that act at excitatory synapses within the central nervous system. Neuronal

responses to glutamate are complex and appear to be mediated by at least three different receptor types, *i.e.*, KA, QA and NMDA subtypes, each being named for their relatively specific ligands, *i.e.*, kainic acid, quisaqualic acid and N-methyl-D-aspartic acid, respectively.

The recognition site, *i.e.*, the NMDA receptor, is external to the ion channel. When glutamate interacts with the NMDA receptor, it causes the ion channel to open, thereby permitting a flow of cations across the cell membrane, *e.g.*, Ca^{2+} and Na^{+} into the cell and K^{+} out of the cell. It is believed that this flux of ions, especially the influx of Ca^{2+} ions, caused by the interaction of glutamate with the NMDA receptor, plays an important role in nerve cell death.

Many diseases are caused by mutations in ion channel genes including, but not limited to, epilepsy and nerve cell degeneration in cases of hypoxia, hypoglycemia, brain or spinal chord ischemia, brain or spinal chord trauma and in neurodegenerative diseases (*e.g.*, Parkinson's disease), Huntington's disease, Down's Syndrome, Amyotrophic Lateral Sclerosis (ALS), Alzheimer's disease, Korsakoff's disease, renal tubular disorders, cystic fibrosis, osteoporosis, Bartter's syndrome, Andersen Syndrome, hyperkinaesia, Spastic Paraplegia, inheritable forms of manic depression, Angelman Syndrome, Febrile seizures, Jervell & Lange-Nielson Syndrome, Romano-Ward Syndrome, Long QT Syndrome 5, Long QT Syndrome 6, Primary hypomagnesemia, hypomagnesemia with secondary hypocalcemia, magnesium and potassium depletion (Gitelman Syndrome), and hypomagnesemia and schizophrenia, as well as others.

With the availability of complete genomic sequences for many organisms today, including *Homo sapiens*, it has become clear that there is a need for data mining techniques to extract the information in them, *e.g.*, gene prediction programs. Of these, the most successful ones are those based on the comparison of known protein or protein-derived information, or those that use expressed sequence tags (ESTs) to predict gene location and structure.

One such algorithm is GeneWise. It bases its exon prediction on the use of Hidden Markov Models (HMMs) of proteins to be compared against a genomic sequence, so that the translation of the sequence will match the model in a similar way to other HMM profile searches (Eddy, *Curr. Opin. Struct. Biol.* 6(3):361-5 (1996), and allowing the presence of long insertions as long as they include donor and acceptor site sequences at both ends.

To take advantage of the algorithm, the models for different protein families must be built so that they represent the full-length sequences instead of the most

common features in them. This is a major difference with existing HMM databases such as Pfam (Sonnhammer *et al.*, *Proteins* 28(3):405-20 (1997), in which each model is built to represent a family of proteins as broad as possible with minimum overlap between them.

In the present approach, the sequences were subdivided in several families so that the similarity inside of a group of them was over 50%. Given this approach, there are several points of overlap between different families when analyzing a sequence, so the discrimination must be done after the search is completed.

Several resources that include expert-supervised classifications are used to select the best groups of sequences, *e.g.*, The Ligand Gated-Ion Channel Receptor Database, NMDA (Weizmann), NuclearR Database (Horn *et al.*, *Nucleic Acids Res.* 29:346-349 (2001)), IOCH (Le Novere *et al.*, *Nucleic Acids Res.* 27(1):340-2 (1999)), Enzyme (Bairoch, *Nucleic Acids Res.* 28:304-305 (2000)) and Swiss-Prot (Bairoch *et al.*, *Nucleic Acids Res.* 28:45-48 (2000)). When none is available, or the sequences included in some groups are too distantly related, the grouping must be done manually, using the ClustalW (Thompson *et al.*, *Nucleic Acids Res.* 22:4673-4680 (1994)) package to measure the distance between different sequences.

The present model was built from multiple sequence alignments of the different protein families obtained with DiAlign 2 (Morgenstern, *Bioinformatics* 15(3):211-8 (1999)). DiAlign works based on segment-to-segment comparisons instead of arbitrary thresholds for gap opening and extension, which makes it ideally suited for building models that represent an entire, full-length sequence, since the alignments built this way have more match states that would be assigned as insertion states when using other alignment algorithms. The models were built using the standard HMMer package.

To search for new genes, a genome-wide scan was done on the University of California at Santa Cruz sequences, using the GeneWise algorithm. It translates the genomic sequence on the fly to proteins and can therefore maintain a reading frame through insertions and deletions. The algorithm also rewards gaps in the genomic sequence relative to the model if they are encapsulated within introns, like splice structure.

For each superfamily of proteins, a classification was obtained in which the sequences are grouped by length and similarity. Each one of these groups was then used to build a HMM profile representing this group of sequences. This approach aims to have models that can represent the full length of the encoded proteins for a whole range of proteins, without being too specific for any one of them or being too

general, as would be a HMM built for large groups of sequences. This classification was based either on existing expert-supervised classifications, or by retrieval of sequences and classification based on pairwise alignment distances.

These models were then searched against the October fixed release of the Santa Cruz contigs using the Paracel GeneMatcher+ Hardware Accelerator with the GeneWise algorithm. The sequences were chopped at 100 Kb with an overlap of 1 Kb. Each one of the superfamilies required between 3 and 6 days to complete and generate results. The results represent the coding regions of the complete final protein as it is found in the organism.

The cross-validation of the results was done in two steps. First, all of the hits with an E-value lower than 10^{-8} that do not overlap with one another were selected, and in the event of overlapping, the one with lowest E-value was selected. After selecting all of those matches, the DNA sequences were compared against the RefSeq database (Pruitt *et al.*, *Trends Genet.* 16(1):44-47 (2000)) using BLAST (Altschul *et al.*. *Nucleic Acids Res.* 25:3389-3402 (1997)).

Over 80% of the sequences were 90% or more identical to an existing human RefSeq entry. The differences are usually due to picking the wrong model for a certain sequence that appears as a hit more than once in different families, being a different valid splice variant, which can be tested by comparing to the EST database, or by addition of a small last exon to complete the match instead of accept an stop codon in a previous one. In all of such cases, the results are easily and quickly corrected by eye. Very rarely the algorithm will actually make a wrong prediction, which is consistent with the expected behaviour (Guigo *et al.*, *Genome Res.* 10(10):1631-42 (2000)).

Of the remaining sequences, over 50% have a match over 90% identical in the public domain protein databases, and the differences between those sequences in the databases and the potential translations is basically the same as the differences between the DNA sequences and the RefSeq entries.

The full sequences of the ion channel genes and splice variants are shown in Table I as SEQ ID NOs:1, 3, 5, 7 and 9. The amino acids encoded by these nucleic acids are shown in Table I as SEQ ID NOs:2, 4, 6, 8 and 10.

A number of the genes were found to be linked with markers known to be associated with human diseases genes. These are shown in Table III. The diseases were linked to the HMM genes in the following manner: (1) the HMM gene models were compared to the consensus of the human genome sequence, located and the results kept in a relational database; (2) all possible markers (Sequence Tagged Sites

(STS's)) (public or deCODE genetics) are also located in the same consensus using ePCR or BLAT and results kept in a relational database; and (3) LOD scores for diseases are linked to markers. A span of one LOD drop around the marker was also given. A computer program takes each LOD peak and links it to the consensus through the markerhit in the database. The database is then queried for all HMM genes within the span of one LOD drop or a minimum of 15 Mb in each direction from the marker. The output is the name of the peak marker and its distance to the HMM gene.

NUCLEIC ACIDS OF THE INVENTION

Accordingly, the invention pertains to isolated nucleic acid molecules comprising human ion channel genes. The term, "ion channel gene", as used herein, refers to an isolated nucleic acid molecule selected from the group shown in Table I, and consisting of SEQ ID NOs:1, 3, 5, 7 and 9, and also to a portion or fragment of the isolated nucleic acid molecule (*e.g.*, cDNA or the gene) that encodes ion channel polypeptide (*e.g.*, a polypeptide selected from the group shown in Table I, and consisting of SEQ ID NOs:2, 4, 6, 8 and 10). In a preferred embodiment, the isolated nucleic acid molecule comprises a nucleic acid molecule selected from the group consisting of SEQ ID NOs:1, 3, 5, 7 and 9 or the complement of such a nucleic acid molecule.

The isolated nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can be double-stranded or single-stranded; single stranded RNA or DNA can be either the coding, or sense, strand or the non-coding, or antisense, strand. The nucleic acid molecule can include all or a portion of the coding sequence of the gene and can further comprise additional non-coding sequences such as introns and non-coding 3' and 5' sequences (including regulatory sequences, for example). Additionally, the nucleic acid molecule can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include, but are not limited to, those that encode a glutathione-S-transferase (GST) fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids that normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (*e.g.*, as in an RNA library). For example, an isolated nucleic

acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules that are separated from the chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated. Thus, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention. An isolated nucleic acid molecule or nucleotide sequence can include a nucleic acid molecule or nucleotide sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleotide sequences include recombinant DNA molecules in heterologous organisms, as well as partially or substantially purified DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleotide sequences. Such isolated nucleotide sequences are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (*e.g.*, from other mammalian species), for gene mapping (*e.g.*, by *in situ* hybridization with chromosomes), or for detecting expression of the gene in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which are not necessarily found in nature but which encode an ion channel polypeptide (*e.g.*, a polypeptide having an amino acid sequence comprising an amino acid sequence

selected from the group consisting of SEQ ID NOs:2, 4, 6, 8 and 10), or another splicing variant of an ion channel polypeptide or polymorphic variant thereof. Thus, for example, DNA molecules which comprise a sequence that is different from the naturally-occurring nucleotide sequence but which, due to the degeneracy of the genetic code, encode an ion channel polypeptide of the present invention are also the subject of this invention. The invention also encompasses nucleotide sequences encoding portions (fragments), or encoding variant polypeptides such as analogues or derivatives of an ion channel polypeptide. Such variants can be naturally-occurring, such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more nucleotides that can result in conservative or non-conservative amino acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they do not alter the characteristics or activity of an ion channel polypeptide. In one preferred embodiment, the nucleotide sequences are fragments that comprise one or more polymorphic microsatellite markers. In another preferred embodiment, the nucleotide sequences are fragments that comprise one or more single nucleotide polymorphisms in an ion channel gene.

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates), charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to a designated sequence via hydrogen bonding and other chemical interactions. Such molecules include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

The invention also pertains to nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide sequence described herein (*e.g.*, nucleic acid molecules which specifically hybridize to a nucleotide sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence

comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7 and 9. In another embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of SEQ ID NOs:2, 4, 6, 8 and 10 or a polymorphic variant thereof. In a preferred embodiment, the variant that hybridizes under high stringency hybridizations has an activity of an ion channel.

Such nucleic acid molecules can be detected and/or isolated by specific hybridization (*e.g.*, under high stringency conditions). "Specific hybridization," as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (*e.g.*, when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a sample wherein the hybridization is to be performed). "Stringency conditions" for hybridization is a term of art which refers to the incubation and wash conditions, *e.g.*, conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (*i.e.*, 100%) complementary to the second, or the first and second may share some degree of complementarity which is less than perfect (*e.g.*, 70%, 75%, 85%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. "High stringency conditions", "moderate stringency conditions" and "low stringency conditions" for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, (1998), the entire teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (*e.g.*, 0.2X SSC, 0.1X SSC), temperature (*e.g.*, room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules. Typically, conditions are used such that sequences at least about 60%, at least about 70%, at

least about 80%, at least about 90% or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize (*e.g.*, selectively) with the most similar sequences in the sample can be determined.

Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200:546-556 (1991), and in, Ausubel, *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, (1998), which describes the determination of washing conditions for moderate or low stringency conditions. Washing is the step in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by which the final wash temperature is reduced (holding SSC concentration constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that hybridize. Generally, doubling the concentration of SSC results in an increase in T_m of -17°C. Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought.

For example, a low stringency wash can comprise washing in a solution containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate stringency wash can comprise washing in a prewarmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in prewarmed (68°C) solution containing 0.1X SSC/0.1%SDS for 15 minutes at 68°C. Furthermore, washes can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

The percent identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first sequence). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 60%, and even more

preferably at least 70%, 80%, 90% or 95% of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl. Acad. Sci. USA* 90:5873-5877 (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used. In one embodiment, parameters for sequence comparison can be set at score=100, word-length=12, or can be varied (*e.g.*, W=5 or W=20).

Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, *CABIOS* 4(1):11-17 (1988). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (Accelrys, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12 , and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti, *Comput. Appl. Biosci.* 10:3-5 (1994); and FASTA described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-8 (1988).

In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software package using either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package using a gap weight of 50 and a length weight of 3.

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7 and 9, or the complement of such a sequence, and also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence encoding an amino acid sequence selected SEQ ID NOs:2, 4, 6, 8 and 10, or polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, preferably at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100,

200 or more nucleotides in length. Longer fragments, for example, 30 or more nucleotides in length, which encode antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers" are oligonucleotides that hybridize in a base-specific manner to a complementary strand of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.*, *Science* 254:1497-1500 (1991).

Typically, a probe or primer comprises a region of nucleotide sequence that hybridizes to at least about 15, typically about 20-25, and more typically about 40, 50 or 75, consecutive nucleotides of a nucleic acid molecule comprising a contiguous nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7 and 9, or the complement of such a sequence, or a sequence encoding an amino acid sequence selected from SEQ ID NOs:2, 4, 6, 8 and 10, or polymorphic variant thereof. In preferred embodiments, a probe or primer comprises 100 or fewer nucleotides, preferably from 6 to 50 nucleotides, preferably from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence, preferably at least 80% identical, more preferably at least 90% identical, even more preferably at least 95% identical, or even capable of selectively hybridizing to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer further comprises a label, *e.g.*, radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated by the polymerase chain reaction using synthetic oligonucleotide primers designed based on one or more of the sequences selected from the group consisting of SEQ ID NOs:1, 3, 5, 7 and 9, or the complement of such a sequence, or designed based on nucleotides based on sequences encoding one or more of the amino acid sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19:4967 (1991); Eckert *et al.*, *PCR Methods and Applications*

1:17 (1991); PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be radiolabelled and used as a probe for screening a cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a polypeptide of the appropriate molecular weight. For example, the direct analysis of the nucleotide sequence of nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Using these or similar methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of one or more of SEQ ID NOs:1, 3, 5, 7 and 9 and/or the complement of one or more of SEQ ID NOs:1, 3, 5, 7 and 9, and/or a portion of one or more of SEQ ID NOs:1, 3, 5, 7 and 9, or the complement of one or more of SEQ ID NOs:1, 3, 5, 7 and 9 and/or a sequence encoding the amino acid sequences of one or more of SEQ ID NOs:2, 4, 6, 8 and 10, or encoding a portion of one or more of SEQ ID NOs:2, 4, 6, 8 and 10, and constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to

increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid molecule will be of an antisense orientation to a target nucleic acid of interest).

In general, the isolated nucleic acid sequences of the invention can be used as molecular weight markers on Southern gels, and as chromosome markers that are labeled to map related gene positions. The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of the disorders described above, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or diagnostic assays described herein, and can also be included as components of kits (*e.g.*, reagent kits) for use in the screening and/or diagnostic assays described herein.

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule selected from the group consisting of SEQ ID NOs:1, 3, 5, 7 and 9 and the complements thereof (or a portion thereof). Yet another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule encoding an amino acid sequence of SEQ ID NOs:2, 4, 6, 8 and 10 or polymorphic variant thereof. The constructs comprise a vector (*e.g.*, an expression vector) into which a sequence of the invention has been inserted in a sense or antisense

orientation. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

Preferred recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid molecule in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" or "operatively linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, "Gene Expression Technology", *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The expression vectors of the invention can be introduced into

host cells to thereby produce polypeptides, including fusion polypeptides, encoded by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, *e.g.*, bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic acid molecule of the invention can be expressed in bacterial cells (*e.g.*, *E. coli*), insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid molecules encoding a selectable

marker can be introduced into a host cell on the same vector as the nucleic acid molecule of the invention or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid molecule can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the invention has been introduced (*e.g.*, an exogenous ion channel gene, or an exogenous nucleic acid encoding an ion channel polypeptide). Such host cells can then be used to create non-human transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleotide sequence and polypeptide encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal include a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Pat. No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, *Current Opinion in BioTechnology* 2:823-829 (1991) and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.*, *Nature* 385:810-813 (1997) and PCT Publication Nos. WO 97/07668 and WO 97/07669.

POLYPEPTIDES OF THE INVENTION

The present invention also pertains to isolated polypeptides encoded by ion channels ("ion channel polypeptides") and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (*e.g.*, other splicing variants). The term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined to another polypeptide with which it is not normally associated in a cell (*e.g.*, in a "fusion protein") and still be "isolated" or "purified."

The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of considerable amounts of other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes preparations of the polypeptide having less than about 30% (by dry weight) other proteins (*i.e.*, contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins.

When a polypeptide is recombinantly produced, it can also be substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7 and 9, or the complement of such a nucleic acid, or portions thereof, *e.g.*, SEQ ID NO:2, 4, 6, 8 and 10, or a portion or polymorphic variant thereof. However, the polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism, *i.e.*, an allelic variant, as well as other splicing variants. Variants also encompass polypeptides derived from other genetic loci in an organism, but having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 3, 5, 7 and 9, or a complement of such a sequence, or portions thereof, or having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of nucleotide sequences encoding SEQ ID NOs:2, 4, 6, 8 and 10, or polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are substantially homologous or identical when the amino acid sequences are at least about 45-55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically greater than about 90% or more homologous or identical.

A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to one or more of SEQ ID NOs:1, 3, 5, 7 and 9, or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding one of SEQ ID NOs:2, 4, 6, 8 and 10, a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

To determine the percent homology or identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one polypeptide or nucleic acid molecule for optimal alignment with the other polypeptide or nucleic acid molecule). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity". The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, percent homology equals the number of identical positions/total number of positions times 100).

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by a polypeptide encoded by a nucleic acid molecule of the invention. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. Further, variant polypeptides can be fully functional or

can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol. 224*:899-904 (1992); de Vos *et al.*, *Science 255*:306-312 (1992)).

The invention also includes polypeptide fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a nucleic acid molecule comprising one of SEQ ID NOs:1, 3, 5, 7 and 9, or a complement of such a nucleic acid (*e.g.*, SEQ ID NOs:2, 4, 6, 8 and 10, or other variants). However, the invention also encompasses fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6 contiguous amino acids. Useful fragments include those that retain one or more of the biological activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain, segment, or motif that has been identified by analysis of the polypeptide sequence using well-known methods, *e.g.*, signal peptides, extracellular domains, one or more transmembrane segments or loops, ligand binding regions, zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one embodiment a fragment designed for

expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

The invention thus provides chimeric or fusion polypeptides. These comprise a polypeptide of the invention operatively linked to a heterologous protein or polypeptide having an amino acid sequence not substantially homologous to the polypeptide. "Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect function of the polypeptide *per se*. For example, the fusion polypeptide can be a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides include, but are not limited to, enzymatic fusion polypeptides, for example □-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of a polypeptide can be increased by using a heterologous signal sequence. Therefore, in another embodiment, the fusion polypeptide contains a heterologous signal sequence at its N-terminus.

EP-A-O 464 533 discloses fusion proteins comprising various portions of immunoglobulin constant regions. The Fc is useful in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). In drug discovery, for example, human proteins have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists. Bennett *et al.*, *Journal of Molecular Recognition, 8*:52-58 (1995) and Johanson *et al.*, *The Journal of Biological Chemistry, 270*,16:9459-9471 (1995). Thus, this invention also encompasses soluble fusion polypeptides containing a polypeptide of the invention and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclass (IgG, IgM, IgA, IgE).

A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to

complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST protein). A nucleic acid molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

The isolated polypeptide can be purified from cells that naturally express it, purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods. In one embodiment, the polypeptide is produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the polypeptide is cloned into an expression vector, the expression vector introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

In general, polypeptides of the present invention can be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using art-recognized methods. The polypeptides of the present invention can be used to raise antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the corresponding polypeptide is preferentially expressed, either constitutively, during tissue differentiation, or in a diseased state. The polypeptides can be used to isolate a corresponding binding agent, *e.g.*, ligand, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction.

ANTIBODIES OF THE INVENTION

Polyclonal and/or monoclonal antibodies that specifically bind one form of the gene product but not to the other form of the gene product are also provided. Antibodies are also provided which bind a portion of either the variant or the reference gene product that contains the polymorphic site or sites. The invention provides antibodies to the polypeptides and polypeptide fragments of the invention, *e.g.*, having an amino acid sequence of one of SEQ ID NOs:2, 4, 6, 8 and 10 or a portion thereof, or having an amino acid sequence encoded by a nucleic acid

molecule comprising all or a portion of SEQ ID NOs:1, 3, 5, 7 and 9, or a complement or another variant or portion thereof. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and $F(ab')_2$ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, *Nature* 256:495-497 (1975), the human B cell hybridoma technique (Kozbor *et al.*, *Immunol. Today* 4:72 (1983)), the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, 1985, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.* (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of

the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal antibody to a polypeptide of the invention (see, *e.g.*, *Current Protocols in Immunology, supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *Surf*ZAP™ Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9:1370-1372 (1991); Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246:1275-1281 (1989); Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (*e.g.*, a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a

polypeptide of the invention can be used to detect the polypeptide (*e.g.*, in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, □-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

DIAGNOSTIC AND SCREENING ASSAYS OF THE INVENTION

The present invention also pertains to a method of diagnosing or aiding in the diagnosis of a disease or condition associated with an ion channel gene or gene product in an individual. Diagnostic assays can be designed for assessing ion channel gene expression, or for assessing activity of ion channel polypeptides of the invention. In one embodiment, the assays are used in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or condition associated with an ion channel, or a defect in an ion channel. The invention also provides for prognostic (or predictive) assays for determining whether an individual is susceptible to a disease of condition associated with an ion channel. For example, mutations in the gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of symptoms associated with a susceptibility to a disease or condition associated with an ion channel. Another aspect of the invention pertains to assays for monitoring the influence of agents (*e.g.*, drugs, compounds or other agents) on the gene expression or activity of polypeptides of the invention, as well as to assays for identifying agents which bind to a polypeptides. These and other assays and agents are described in further detail in the following sections.

DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of a susceptibility to a disease or condition associated with an ion channel, as well as in kits useful for diagnosis of a susceptibility to a disease or condition associated with an ion channel.

In one embodiment of the invention, diagnosis of a susceptibility to a disease or condition associated with an ion channel is made by detecting a polymorphism in an ion channel as described herein. The polymorphism can be a mutation in an ion channel, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift mutation; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of the gene; duplication of all or a part of the gene; transposition of all or a part of the gene; or rearrangement of all or a part of the gene. More than one such mutation may be present in a single gene. Such sequence changes cause a mutation in the polypeptide encoded by an ion channel gene. For example, if the mutation is a frame shift mutation, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a susceptibility to a disease or condition associated with an ion channel can be a synonymous mutation in one or more nucleotides (*i.e.*, a mutation that does not result in a change in the polypeptide encoded by an ion channel gene). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the gene. An ion channel gene that has any of the mutations described above is referred to herein as a "mutant gene."

In a first method of diagnosing a susceptibility to a susceptibility to a disease or condition associated with an ion channel, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, including all supplements through 1999). For example, a biological sample from a test subject (a "test sample") of genomic DNA, RNA, or cDNA, is obtained

from an individual suspected of having, being susceptible to or predisposed for, or carrying a defect for, a susceptibility to a disease or condition associated with an ion channel (the "test individual"). The individual can be an adult, child, or fetus. The test sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a polymorphism in an ion channel is present, and/or to determine which splicing variant(s) encoded by the ion channel is present. The presence of the polymorphism or splicing variant(s) can be indicated by hybridization of the gene in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A "nucleic acid probe", as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain at least one polymorphism in an ion channel or contains a nucleic acid encoding a particular splicing variant of an ion channel. The probe can be any of the nucleic acid molecules described above (*e.g.*, the gene, a fragment, a vector comprising the gene, a probe or primer, etc.).

To diagnose a susceptibility to a susceptibility to a disease or condition associated with an ion channel, a hybridization sample is formed by contacting the test sample containing an ion channel with at least one nucleic acid probe. A preferred probe for detecting mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length nucleic acid molecule, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs:1, 3, 5, 7 and 9, or the complement thereof, or a portion thereof; or can be a nucleic acid encoding a portion of one of SEQ ID NOs:2, 4, 6, 8 and 10. Other suitable probes for use in the diagnostic assays of the invention are described above (see *e.g.*, probes and primers discussed under the heading, "Nucleic Acids of the Invention").

The hybridization sample is maintained under conditions that are sufficient to allow specific hybridization of the nucleic acid probe to an ion channel. "Specific hybridization", as used herein, indicates exact hybridization (*e.g.*, with no mismatches). Specific hybridization can be performed under high stringency

conditions or moderate stringency conditions, for example, as described above. In a particularly preferred embodiment, the hybridization conditions for specific hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and the ion channel in the test sample, then the ion channel has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the ion channel, or of the presence of a particular splicing variant encoding the ion channel and is therefore diagnostic for a susceptibility to a susceptibility to a disease or condition associated with an ion channel.

In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, *supra*) the hybridization methods described above are used to identify the presence of a polymorphism or a particular splicing variant, associated with a susceptibility to a susceptibility to a disease or condition associated with an ion channel. For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a nucleic acid probe, as described above, to RNA from the individual is indicative of a polymorphism in an ion channel, or of the presence of a particular splicing variant encoded by an ion channel, and is therefore diagnostic for a susceptibility to a susceptibility to a disease or condition associated with an ion channel.

For representative examples of use of nucleic acid probes, see, for example, U.S. Patents No. 5,288,611 and 4,851,330.

Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P.E. *et al.*, *Bioconjugate Chemistry* 5, American Chemical Society, p. 1 (1994). The PNA probe can be designed to specifically hybridize to a gene having a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with an ion channel. Hybridization of the PNA probe to an ion channel is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with an ion channel.

In another method of the invention, mutation analysis by restriction digestion can be used to detect a mutant gene, or genes containing a polymorphism(s), if the mutation or polymorphism in the gene results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify an ion channel (and, if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology, supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the mutation or polymorphism in the ion channel, and therefore indicates the presence or absence of this susceptibility to a susceptibility to a disease or condition associated with an ion channel.

Sequence analysis can also be used to detect specific polymorphisms in an ion channel. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the gene, and/or its flanking sequences, if desired. The sequence of an ion channel, or a fragment of the gene, or cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA, is determined, using standard methods. The sequence of the gene, gene fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known nucleic acid sequence of the gene, cDNA (*e.g.*, one or more of SEQ ID NOs:1, 3, 5, 7 and 9, or a complement thereof, or a nucleic acid sequence encoding one of SEQ ID NOs:2, 4, 6, 8 and 10 or a fragment thereof) or mRNA, as appropriate. The presence of a polymorphism in the ion channel indicates that the individual has a susceptibility to a susceptibility to a disease or condition associated with an ion channel.

Allele-specific oligonucleotides can also be used to detect the presence of a polymorphism in an ion channel, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, preferably approximately 15-30 base pairs, that specifically hybridizes to an ion channel, and that contains a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with an ion channel. An allele-specific oligonucleotide probe that is specific for particular polymorphisms in an ion channel can be prepared, using standard methods (see *Current Protocols in Molecular Biology, supra*). To identify polymorphisms in the gene that are associated with a

susceptibility to a susceptibility to a disease or condition associated with an ion channel, a test sample of DNA is obtained from the individual. PCR can be used to amplify all or a fragment of an ion channel, and its flanking sequences. The DNA containing the amplified ion channel (or fragment of the gene) is dot-blotted, using standard methods (see *Current Protocols in Molecular Biology*, *supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the amplified ion channel is then detected. Specific hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the ion channel, and is therefore indicative of a susceptibility to a susceptibility to a disease or condition associated with an ion channel.

In another embodiment, arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in an ion channel. For example, in one embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. These oligonucleotide arrays, also described as "Genechips™," have been generally described in the art, for example, U.S. Pat. No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092. These arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods that incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See Fodor *et al.*, *Science* 251:767-777 (1991), Pirrung *et al.*, U.S. Pat. No. 5,143,854 (see also PCT Application No. WO 90/15070) and Fodor *et al.*, PCT Publication No. WO 92/10092 and U.S. Pat. No. 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, *e.g.*, U.S. Pat. Nos. 5,384,261, the entire teachings of which are incorporated by reference herein.

Once an oligonucleotide array is prepared, a nucleic acid of interest is hybridized with the array and scanned for polymorphisms. Hybridization and scanning are generally carried out by methods described herein and also in, *e.g.*, published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. No. 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence that includes one or more previously identified polymorphic markers is amplified by well known amplification techniques, *e.g.*, PCR. Typically, this involves the use of primer sequences that are complementary to the two strands of the target sequence both upstream and

downstream from the polymorphism. Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array.

Although primarily described in terms of a single detection block, *e.g.*, for detection of a single polymorphism, arrays can include multiple detection blocks, and thus be capable of analyzing multiple, specific polymorphisms. In alternate arrangements, it will generally be understood that detection blocks may be grouped within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of those polymorphisms that fall within G-C rich stretches of a genomic sequence, separately from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional description of use of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Patents 5,858,659 and 5,837,832, the entire teachings of which are incorporated by reference herein. Other methods of nucleic acid analysis can be used to detect polymorphisms in an ion channel or variants encoding by an ion channel. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1988); Sanger, F. *et al.*, *Proc. Natl. Acad. Sci. USA* 74:5463-5467 (1977); Beavis *et al.* U.S. Pat. No. 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:232-236 (1989)), mobility shift analysis (Orita, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al.*, *Cell* 15:25 (1978); Geever, *et al.*, *Proc. Natl. Acad. Sci. USA* 78:5081 (1981)); heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection assays (Myers, R.M. *et al.*, *Science* 230:1242 (1985)); use of polypeptides which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

In another embodiment of the invention, diagnosis of a susceptibility to a susceptibility to a disease or condition associated with an ion channel can also be made by examining expression and/or composition of an ion channel polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by an ion channel, or for the presence of a particular variant encoded by an ion channel. An alteration in expression of a polypeptide encoded by an ion channel can be, for example, an alteration in the quantitative polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a polypeptide encoded by an ion channel is an alteration in the qualitative polypeptide expression (*e.g.*, expression of a mutant ion channel polypeptide or of a different splicing variant). In a preferred embodiment, diagnosis of a susceptibility to a susceptibility to a disease or condition associated with an ion channel is made by detecting a particular splicing variant encoded by that ion channel, or a particular pattern of splicing variants.

Both such alterations (quantitative and qualitative) can also be present. An "alteration" in the polypeptide expression or composition, as used herein, refers to an alteration in expression or composition in a test sample, as compared with the expression or composition of polypeptide by an ion channel in a control sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from an individual who is not affected by a susceptibility to a disease or condition associated with an ion channel. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, is indicative of a susceptibility to a susceptibility to a disease or condition associated with an ion channel. Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a susceptibility to a susceptibility to a disease or condition associated with an ion channel. Various means of examining expression or composition of the polypeptide encoded by an ion channel can be used, including spectroscopy, colorimetry, electrophoresis, isoelectric focusing, and immunoassays (*e.g.*, David *et al.*, U.S. Pat. No. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one embodiment, an antibody capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or

more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or $F(ab')_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by a mutant ion channel, or an antibody that specifically binds to a polypeptide encoded by a non-mutant gene, or an antibody that specifically binds to a particular splicing variant encoded by an ion channel, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or mutant ion channel, or the absence in a test sample of a particular splicing variant or of a polypeptide encoded by a non-polymorphic or non-mutant gene. The presence of a polypeptide encoded by a polymorphic or mutant gene, or the absence of a polypeptide encoded by a non-polymorphic or non-mutant gene, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with an ion channel, as is the presence (or absence) of particular splicing variants encoded by the ion channel gene.

In one embodiment of this method, the level or amount of polypeptide encoded by an ion channel in a test sample is compared with the level or amount of the polypeptide encoded by the ion channel in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the ion channel, and is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that ion channel. Alternatively, the composition of the polypeptide encoded by an ion channel in a test sample is compared with the composition of the polypeptide encoded by the ion channel in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide in the test sample, as compared with the composition of the polypeptide in the control sample, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that ion channel. In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample

and in the control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a susceptibility to a susceptibility to a disease or condition associated with that ion channel.

Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as decribed herein (*e.g.*, labeled probes or primers), reagents for detection of labeled molecules, restriction enzymes (*e.g.*, for RFLP analysis), allele-specific oligonucleotides, antibodies which bind to mutant or to non-mutant (native) ion channel polypeptide, means for amplification of nucleic acids comprising an ion channel, or means for analyzing the nucleic acid sequence of an ion channel or for analyzing the amino acid sequence of an ion channel polypeptide, etc.

SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

The invention provides methods (also referred to herein as "screening assays") for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs:1, 3, 5, 7 and 9, or the complement thereof, or a nucleic acid encoding an amino acid having the sequence of one of SEQ ID NOs:2, 4, 6, 8 and 10, or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In a preferred embodiment, high stringency conditions are conditions appropriate for selective hybridization. In another embodiment, a sample containing the nucleic acid molecule of interest is contacted with a nucleic acid containing a contiguous nucleotide sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of the nucleic acid molecule of interest (*e.g.*, an ion channel nucleic acid), and the contacted sample is assessed for the presence or absence of hybridization. In a preferred embodiment, the nucleic acid containing a contiguous nucleotide sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be subjected to amplification prior to performing the hybridization.

In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described above), and then assessing the sample for the presence (or absence) of binding of the antibody to the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes which alter (*e.g.*, increase or decrease) the activity of the polypeptides described herein, or which otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (*e.g.*, ion channel binding agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which change (*e.g.*, enhance or inhibit) the ability of the polypeptides of the invention to interact with ion channel binding agents (*e.g.*, receptors or other binding agents); or which alter posttranslational processing of the ion channel polypeptide (*e.g.*, agents that alter proteolytic processing to direct the polypeptide from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.

In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays. Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of an ion channel polypeptide, a cell, cell lysate, or solution containing or expressing an ion channel polypeptide (*e.g.*, one of SEQ ID NOs:2, 4, 6, 8 and 10, or another splicing

variant encoded by an ion channel), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of ion channel activity is assessed (*e.g.*, the level (amount) of ion channel activity is measured, either directly or indirectly), and is compared with the level of activity in a control (*i.e.*, the level of activity of the ion channel polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of an ion channel polypeptide. An increase in the level of ion channel activity relative to a control, indicates that the agent is an agent that enhances (is an agonist of) ion channel activity. Similarly, a decrease in the level of ion channel activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) ion channel activity. In another embodiment, the level of activity of an ion channel polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters ion channel activity.

The present invention also relates to an assay for identifying agents which alter the expression of an ion channel gene (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the gene or which otherwise interact with the nucleic acids described herein, as well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding an ion channel polypeptide (*e.g.*, an ion channel gene) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution can be another solution that comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of ion channel expression (*e.g.*, the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level and/or pattern of expression in a control (*i.e.*, the level and/or pattern of the ion channel expression in the absence of the agent to be tested). If the level and/or

pattern in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of an ion channel. Enhancement of ion channel expression indicates that the agent is an agonist of ion channel activity. Similarly, inhibition of ion channel expression indicates that the agent is an antagonist of ion channel activity. In another embodiment, the level and/or pattern of ion channel polypeptide(s) (*e.g.*, different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that has previously been established. A level and/or pattern in the presence of the agent that differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters ion channel expression.

In another embodiment of the invention, agents which alter the expression of an ion channel gene or which otherwise interact with the nucleic acids described herein, can be identified using a cell, cell lysate, or solution containing a nucleic acid encoding the promoter region of the ion channel gene operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (*e.g.*, the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (*i.e.*, the level of the expression of the reporter gene in the absence of the agent to be tested). If the level in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression of the ion channel, as indicated by its ability to alter expression of a gene that is operably linked to the ion channel gene promoter. Enhancement of the expression of the reporter indicates that the agent is an agonist of ion channel activity. Similarly, inhibition of the expression of the reporter indicates that the agent is an antagonist of ion channel activity. In another embodiment, the level of expression of the reporter in the presence of the agent to be tested, is compared with a control level that has previously been established. A level in the presence of the agent that differs from the control level by an amount or in a manner that is statistically significant indicates that the agent alters f expression.

Agents which alter the amounts of different splicing variants encoded by an ion channel (*e.g.*, an agent which enhances activity of a first splicing variant, and which inhibits activity of a second splicing variant), as well as agents which are agonists of activity of a first splicing variant and antagonists of activity of a second splicing variant, can easily be identified using these methods described above.

In other embodiments of the invention, assays can be used to assess the impact of a test agent on the activity of a polypeptide in relation to an ion channel binding agent. For example, a cell that expresses a compound that interacts with an ion channel (herein referred to as a "ion channel binding agent", which can be a polypeptide or other molecule that interacts with an ion channel, such as a receptor) is contacted with an ion channel in the presence of a test agent, and the ability of the test agent to alter the interaction between the ion channel and the ion channel binding agent is determined. Alternatively, a cell lysate or a solution containing the ion channel binding agent, can be used. An agent which binds to the ion channel or the ion channel binding agent can alter the interaction by interfering with, or enhancing the ability of the ion channel to bind to, associate with, or otherwise interact with the ion channel binding agent. Determining the ability of the test agent to bind to an ion channel or an ion channel binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the polypeptide can be determined by detecting the labeled with ^{125}I, ^{35}S, ^{14}C or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. It is also within the scope of this invention to determine the ability of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent with an ion channel or an ion channel binding agent without the labeling of either the test agent, ion channel, or the ion channel binding agent. McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a "microphysiometer" (*e.g.*, Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between ligand and polypeptide. Thus, these receptors can be used to screen for compounds that are agonists for use in treating a susceptibility to a disease or condition associated with an ion channel or antagonists for studying a susceptibility to a disease or condition associated with an ion channel. Drugs could be designed to regulate ion channel activation that in turn can be used to regulate signaling pathways and transcription events of genes downstream.

In another embodiment of the invention, assays can be used to identify polypeptides that interact with one or more ion channel polypeptides, as described herein. For example, a yeast two-hybrid system such as that described by Fields and Song (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more ion channel polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor that has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different proteins that interact with one another, transcriptional activation can be achieved, and transcription of specific markers (*e.g.*, nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of interaction and transcriptional activation. For example, in the methods of the invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also an ion channel polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the ion channel polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, an ion channel polypeptide binding agent or receptor). Incubation of yeast containing the first vector and the second vector under appropriate conditions (*e.g.*, mating conditions such as used in the Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies that express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the ion channel polypeptide or fragment or derivative thereof. Such polypeptides may be useful as agents that alter the activity of expression of an ion channel polypeptide, as described above.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either the ion channel, the ion channel binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that

allows an ion channel or an ion channel binding agent to be bound to a matrix or other solid support.

In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a nucleic acid encoding an ion channel is contacted with a test agent and the expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test agent is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by methods described herein for detecting mRNA or polypeptide.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a test agent that is a modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an agent identified as described herein can be used to alter activity of a polypeptide encoded by an ion channel, or to alter expression of an ion channel, by contacting the polypeptide or the gene (or contacting a cell comprising the polypeptide or the gene) with the agent identified as described herein.

PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions comprising nucleic acids described herein, particularly nucleotides encoding the polypeptides described herein; comprising polypeptides described herein (*e.g.*, one or more of SEQ ID NOs:2, 4, 6, 8 and 10); and/or comprising other splicing variants encoded by an ion channel; and/or an agent that alters (*e.g.*, enhances or inhibits) ion channel gene expression or ion channel polypeptide activity as described herein. For instance, a polypeptide, protein (*e.g.*, an ion channel receptor), an agent that alters ion channel gene expression, or an ion channel binding agent or binding partner, fragment, fusion protein or prodrug thereof, or a nucleotide or nucleic acid construct (vector) comprising a nucleotide of the present invention, or an agent that alters ion channel polypeptide activity, can be formulated with a physiologically acceptable carrier or excipient to prepare a pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrolidone, etc., as well as combinations thereof. The pharmaceutical preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, polyvinyl pyrollidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of introduction can also include gene therapy (as described below), rechargeable or biodegradable devices, particle acceleration devises ("gene guns") and slow release polymeric devices. The

pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The composition can be formulated in accordance with the routine procedures as a pharmaceutical composition adapted for administration to human beings. For example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

For topical application, nonsprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments, powders, enemas, lotions, sols, liniments, salves, aerosols, etc., which are, if desired, sterilized or mixed with auxiliary agents, *e.g.*, preservatives, stabilizers, wetting agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze bottle or in admixture with a pressurized volatile, normally gaseous propellant, *e.g.*, pressurized air.

Agents described herein can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or

condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms of a susceptibility to a disease or condition associated with an ion channel, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use of sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet. Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is intended to mean a dosage that is dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

METHODS OF THERAPY

The present invention also pertains to methods of treatment (prophylactic and/or therapeutic) for a susceptibility to a disease or condition associated with an ion channel, using an ion channel therapeutic agent. An "ion channel therapeutic agent" is an agent that alters (*e.g.*, enhances or inhibits) ion channel polypeptide activity and/or ion channel gene expression, as described herein (*e.g.*, an ion channel agonist or antagonist). Ion channel therapeutic agents can alter ion channel polypeptide activity or gene expression by a variety of means, such as, for example, by providing additional ion channel polypeptide or by upregulating the transcription or translation of the ion channel gene; by altering posttranslational processing of the ion channel polypeptide; by altering transcription of ion channel splicing variants; or

by interfering with ion channel polypeptide activity (*e.g.*, by binding to an ion channel polypeptide), or by downregulating the transcription or translation of an ion channel gene. Representative ion channel therapeutic agents include the following:

nucleic acids or fragments or derivatives thereof described herein, particularly nucleotides encoding the polypeptides described herein and vectors comprising such nucleic acids (*e.g.*, a gene, cDNA, and/or mRNA, such as a nucleic acid encoding an ion channel polypeptide or active fragment or derivative thereof, or an oligonucleotide; for example, one of SEQ ID NOs:1, 3, 5, 7 and 9, or a complement thereof, or a nucleic acid encoding one of SEQ ID NOs:2, 4, 6, 8 and 10, or fragments or derivatives thereof);

polypeptides described herein (*e.g.*, one or more of SEQ ID NOs:2, 4, 6, 8 and 10, and/or other splicing variants encoded by an ion channel, or fragments or derivatives thereof);

other polypeptides (*e.g.*, ion channel receptors); ion channel binding agents; peptidomimetics; fusion proteins or prodrugs thereof; antibodies (*e.g.*, an antibody to a mutant ion channel polypeptide, or an antibody to a non-mutant ion channel polypeptide, or an antibody to a particular splicing variant encoded by an ion channel, as described above); ribozymes; other small molecules; and

other agents that alter (*e.g.*, enhance or inhibit) ion channel gene expression or polypeptide activity, or that regulate transcription of ion channel splicing variants (*e.g.*, agents that affect which splicing variants are expressed, or that affect the amount of each splicing variant that is expressed.

More than one ion channel therapeutic agent can be used concurrently, if desired.

An ion channel therapeutic agent that is a nucleic acid is used in the treatment of a susceptibility to a disease or condition associated with an ion channel. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease, but also preventing or delaying the onset of the disease, and also lessening the severity or frequency of symptoms of the disease. The therapy is designed to alter (*e.g.*, inhibit or enhance), replace or supplement activity of an ion channel polypeptide in an individual. For example, an ion channel therapeutic agent can be administered in order to upregulate or increase the expression or availability of the ion channel gene or of specific splicing variants of ion channel, or, conversely, to downregulate or decrease the expression or availability of the ion channel gene or specific splicing variants of the ion channel. Upregulation or increasing expression or availability of a native ion channel gene or

of a particular splicing variant could interfere with or compensate for the expression or activity of a defective gene or another splicing variant; downregulation or decreasing expression or availability of a native ion channel gene or of a particular splicing variant could minimize the expression or activity of a defective gene or the particular splicing variant and thereby minimize the impact of the defective gene or the particular splicing variant.

The ion channel therapeutic agent(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease, such as by ameliorating symptoms associated with the disease, preventing or delaying the onset of the disease, and/or also lessening the severity or frequency of symptoms of the disease). The amount which will be therapeutically effective in the treatment of a particular individual's disorder or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In one embodiment, a nucleic acid of the invention (*e.g.*, a nucleic acid encoding an ion channel polypeptide, such as one of SEQ ID NOs:1, 3, 5, 7 and 9, or a complement thereof; or another nucleic acid that encodes an ion channel polypeptide or a splicing variant, derivative or fragment thereof, such as a nucleic acid encoding one of SEQ ID NOs:2, 4, 6, 8 and 10) can be used, either alone or in a pharmaceutical composition as described above. For example, an ion channel or a cDNA encoding an ion channel polypeptide, either by itself or included within a vector, can be introduced into cells (either *in vitro* or *in vivo*) such that the cells produce native ion channel polypeptide. If necessary, cells that have been transformed with the gene or cDNA or a vector comprising the gene or cDNA can be introduced (or re-introduced) into an individual affected with the disease. Thus, cells which, in nature, lack native ion channel expression and activity, or have mutant ion channel expression and activity, or have expression of a disease-associated ion channel splicing variant, can be engineered to express the ion channel polypeptide or an active fragment of the ion channel polypeptide (or a different variant of the ion channel polypeptide). In a preferred embodiment, nucleic acid encoding an ion channel polypeptide, or an active fragment or derivative thereof,

can be introduced into an expression vector, such as a viral vector, and the vector can be introduced into appropriate cells in an animal. Other gene transfer systems, including viral and nonviral transfer systems, can be used. Alternatively, nonviral gene transfer methods, such as calcium phosphate coprecipitation, mechanical techniques (*e.g.*, microinjection); membrane fusion-mediated transfer via liposomes; or direct DNA uptake, can also be used.

Alternatively, in another embodiment of the invention, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (*e.g.*, an oligonucleotide as described below), can be used in "antisense" therapy, in which a nucleic acid (*e.g.*, an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of an ion channel is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the ion channel polypeptide, *e.g.*, by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA that is complementary to a portion of the mRNA and/or DNA which encodes the ion channel polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the ion channel. In one embodiment, the oligonucleotide probes are modified oligonucleotides which are resistant to endogenous nucleases, *e.g.*, exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Pat. Nos. 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.* (*Biotechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the ion channel. The antisense oligonucleotides bind to ion channel mRNA transcripts and prevent translation.

Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.* for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication No. WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *BioTechniques* 6:958-976 (1988)) or intercalating agents. (See, *e.g.*, Zon, Pharm. Res. 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

The antisense molecules are delivered to cells that express ion channel *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systematically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form

complementary base pairs with the endogenous ion channel transcripts and thereby prevent translation of the ion channel mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically).

Endogenous ion channel expression can also be reduced by inactivating or "knocking out" ion channel or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, a mutant, non-functional ion channel (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous ion channel (either the coding regions or regulatory regions of ion channel) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the ion channel *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the ion channel. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above. Alternatively, expression of non-mutant ion channels can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-mutant, functional ion channel, *e.g.*, a gene having one of SEQ ID NOs:1, 3, 5, 7 and 9, or the complement thereof, or a portion thereof, in place of a mutant ion channel in the cell, as described above. In another embodiment, targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes an ion channel polypeptide variant that differs from that present in the cell.

Alternatively, endogenous ion channel expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of an ion channel (*i.e.*, the ion channel promoter and/or enhancers) to form triple helical structures that prevent transcription of the ion channel in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.*, 6(6):569-84 (1991); Helene, C. *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-

15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity of one of the ion channel proteins, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to an ion channel mRNA or gene sequence) can be used to investigate the role of one or ion channel in developmental events, as well as the normal cellular function of the ion channels in adult tissue. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

In yet another embodiment of the invention, other ion channel therapeutic agents as described herein can also be used in the treatment or prevention of a susceptibility to a disease or condition associated with an ion channel. The therapeutic agents can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic agents can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Pat. No. 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein.

A combination of any of the above methods of treatment (*e.g.*, administration of non-mutant ion channel polypeptide in conjunction with antisense therapy targeting mutant ion channel mRNA; administration of a first splicing variant encoded by an ion channel in conjunction with antisense therapy targeting a second splicing encoded by an ion channel), can also be used.

The teachings of all publications cited herein are incorporated herein by reference in their entirety.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

Table I

MOOSE03990 ctg17115 505609..505687, 505992..506156, 508524..508621, 508726..508891, 511852..512030, 514401..514454, 514556..514717, 516907..517059, 517450..517569, 517670..517777, 528624..528827, 549025..549138, 549323..549432, 549905..550078, 564568..564733, 565430..565655, 567696..567824, 567926..568100, 568230..568347

MPAELLLLLIVAFASPSCQVLSSLRMAAILDDQTVCGRGERLALALAR
EQINGIIEVPAKARVEVDIFELQRDSQYETTDTMCQILPKGVVSVLGPSSSPAS
ASTVSHICGEKEIPHIKVGPEETPRLQYLRFASVSLYPSNEDVSLAVSRILKSF
NYPSASLICAKAECLLRLEELVRGFLISKETLSVRMLDDSRDPTPLLKEIRDD
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MOOSE04091 ctg12577 507898..508054, 516506..516531, 529945..529962, 535729..535952, 539252..539334, 540382..540522, 546517..546669, 555236..555396, 557909..558044, 560177..560258, 561311..561597, 561991..561999

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MOOSE04099 ctg19215 786..885, 3635..3660, 5490..5560, 6066..6091, 7773..7793, 8372..8401, 9453..9507, 10020..10066, 10322..10474, 17783..17979, 18283..18342, 22952..23230

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Table II

ctg17115_MOOSE03990.xml GLUka Glutamate Receptor Ion Channel KA Subunit (Kainate)
ctg15547_MOOSE03992.xml GLUka Glutamate Receptor Ion Channel KA Subunit (Kainate)
ctg15811_MOOSE04086.xml GABA Gated Ion Channel Receptor (Vertebrate)
ctg12577_MOOSE04091.xml GABA Gated Ion Channel Receptor (Vertebrate)
ctg19215_MOOSE04099.xml GABA Gated Ion Channel Receptor (Vertebrate)

Table III

ION CHANNELS

##########

Asthma

Locus2 Marker:D3S1546 Lod:3.4 CM RANGE of one LOD drop: 17

MOOSE08125 (MOOSE04091) GABA Gated Ion Channel Receptor (Vertebrate)
DISTANCE: -6.68 Mb

##########

Obesity

Locus5 Marker:SHGC-1089 Lod:4.6 CM RANGE of one LOD drop: 20

MOOSE08126 (MOOSE04099) GABA Gated Ion Channel Receptor (Vertebrate)
DISTANCE: -3.47 Mb

CLAIMS

What is claimed is:

1. An isolated nucleic acid molecule comprising an ion channel gene, wherein the ion channel gene has a nucleotide sequence selected from the group of nucleic acid sequences as shown in Table I, or the complements of the group of nucleic acid sequences as shown in Table I.

2. A nucleic acid encoding a polypeptide, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Table I.

3. An isolated nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group of nucleic acid sequences as shown in Table I, or the complements of the group of nucleic acid sequences as shown in Table I.

4. An isolated nucleic molecule that hybridizes under high stringency conditions to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Table I.

5. A method for assaying for the presence of a first nucleic acid molecule in a sample, comprising contacting said sample with a second nucleic acid molecule, where the second nucleic acid molecule comprises a nucleotide sequence selected from the group of nucleic acid sequences as shown in Table I, and hybridizes to the first nucleic acid under high stringency conditions.

6. A vector comprising an isolated nucleic acid molecule selected from the group consisting of:
   (a) the nucleic acid sequences as shown in Table I;
   (b) the complement of one of the nucleic acid sequences are shown in Table I; or
   (c) a nucleic acid encoding an amino acid molecule as shown in Table I;

   wherein the nucleic acid molecule is operably linked to a regulatory sequence.

7. A recombinant host cell comprising the vector of Claim 6.

8. A method for producing a polypeptide encoded by an isolated nucleic acid molecule, comprising culturing the recombinant host cell of Claim 7 under conditions suitable for expression of the nucleic acid molecule.

9. An isolated polypeptide encoded by the nucleotide sequence of the group of nucleic acid sequences as shown in Table I, or the complements thereof.

10. The isolated polypeptide of Claim 9, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Table I.

11. An isolated polypeptide comprising an amino acid sequence, wherein the amino acid sequence is greater than about 95% identical to an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Table I.

12. A fusion protein comprising an isolated polypeptide of Claim 2.

13. A fusion protein comprising an isolated polypeptide of Claim 11.

14. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 2, or to a fragment or variant of said amino acid sequence.

15. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 11, or to a fragment or variant of said amino acid sequence.

16. A method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule according to Claim 1 in a sample, the method comprising contacting the sample with an antibody which specifically binds to the encoded polypeptide.

17. A method of identifying an agent which alters the activity of an ion channel, the method comprising:

(a) contacting a polypeptide of Claim 9, or a derivative or fragment thereof, with an agent to be tested;

(b) assessing the level of activity of the polypeptide or derivative or fragment thereof; and

(c) comparing the level of activity with a level of activity of the polypeptide or active derivative or fragment thereof in the absence of the agent;

wherein if the level of activity of the polypeptide or derivative or fragment thereof in the presence of the agent differs, by an amount that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters activity of an ion channel.

18. An agent that alters the activity of an ion channel, identifiable according to the method of Claim 17.

19. The agent of Claim 18, where the agent is selected from the group consisting of: an ion channel gene binding agent; a receptor; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.

20. A method of altering activity of a polypeptide encoded by an ion channel gene, comprising contacting the polypeptide with an agent of Claim 19.

21. A method of identifying an agent that alters interaction of the polypeptide of Claim 9 with an ion channel gene binding agent, comprising:

a) contacting the polypeptide or a derivative or fragment thereof, and the binding agent, with an agent to be tested;

b) assessing the interaction of the polypeptide or derivative or fragment thereof with the binding agent; and

c) comparing the level of interaction with a level of interaction of the polypeptide or derivative or fragment thereof with the binding agent in the absence of the agent,

wherein if the level of interaction of the polypeptide or derivative or fragment thereof in the presence of the agent differs by an amount that is statistically significant, from the level of interaction in the absence of the agent, then the

agent is an agent that alters interaction of the polypeptide with the binding agent.

22. An agent which alters interaction of an ion channel gene polypeptide with an ion channel gene binding agent, identifiable according to the method of Claim 21.

23. An agent which alters interaction of an ion channel gene polypeptide with an ion channel gene binding agent, selected from the group consisting of: a second ion channel gene binding agent; a receptor; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.

24. A method of altering interaction of an ion channel gene polypeptide with an ion channel gene binding agent, comprising contacting the ion channel gene polypeptide and/or the ion channel gene binding agent with an agent of Claim 23.

25. A method of identifying an agent that alters expression of an ion channel gene, comprising the steps of:

a) contacting a solution containing a nucleic acid comprising the promoter region of the ion channel gene operably linked to a reporter gene with an agent to be tested;

b) assessing the level of expression of the reporter gene; and

c) comparing the level of expression with a level of expression of the reporter gene in the absence of the agent,

wherein if the level of expression of the reporter gene in the presence of the agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the ion channel gene.

26. An agent that alters expression of the ion channel gene, identifiable according to the method of Claim 25.

27. A method of identifying an agent that alters expression of an ion channel gene, comprising the steps of:

a) contacting a solution containing a nucleic acid of Claim 1 or a derivative or fragment thereof with an agent to be tested;
b) assessing expression of the nucleic acid, derivative or fragment; and
c) comparing expression with expression of the nucleic acid, derivative or fragment in the absence of the agent,

wherein if expression of the nucleotide, derivative or fragment in the presence of the agent differs, by an amount that is statistically significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the ion channel gene.

28. The method of Claim 27, wherein the expression of the nucleotide, derivative or fragment in the presence of the agent comprises expression of one or more splicing variant(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent.

29. An agent that alters expression of an ion channel gene, identifiable according to the method of Claim 27.

30. An agent that alters expression of an ion channel gene, selected from the group consisting of: antisense nucleic acid to an ion channel gene; an ion channel gene polypeptide; an ion channel gene receptor; an ion channel gene binding agent; a peptidomimetic; a fusion protein; a prodrug thereof; an antibody; and a ribozyme.

31. A method of altering expression of an ion channel gene, comprising contacting a cell containing an ion channel gene with an agent of Claim 30.

32. A method of identifying a polypeptide which interacts with an ion channel gene polypeptide, comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and an ion channel gene polypeptide, splicing variant, or a fragment or derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide, wherein if transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide which interacts with an ion channel polypeptide.

33. An ion channel gene therapeutic agent selected from the group consisting of: an ion channel gene or fragment or derivative thereof; a polypeptide encoded by an ion channel gene; a receptor; an ion channel gene binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters ion channel gene expression; an agent that alters activity of a polypeptide encoded by an ion channel gene; an agent that alters posttranscriptional processing of a polypeptide encoded by an ion channel gene; an agent that alters interaction of an ion channel gene with an ion channel gene binding agent; an agent that alters transcription of splicing variants encoded by an ion channel gene; and a ribozyme.

34. A pharmaceutical composition comprising an ion channel gene therapeutic agent of Claim 33.

35. The pharmaceutical composition of Claim 34, wherein the ion channel gene therapeutic agent is an isolated nucleic acid molecule comprising an ion channel gene or fragment or derivative thereof.

36. The pharmaceutical composition of Claim 34, wherein the ion channel gene therapeutic agent is a polypeptide encoded by the ion channel gene.

37. A method of treating a disease or condition associated with an ion channel in an individual, comprising administering an ion channel gene therapeutic agent to the individual, in a therapeutically effective amount.

38. The method of Claim 37, wherein the ion channel gene therapeutic agent is an ion channel gene agonist.

39. The method of Claim 38 wherein the ion channel gene therapeutic agent is an ion channel gene antagonist.

40. A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous ion channel gene and a nucleic acid encoding an ion channel gene polypeptide.

41. A method for assaying a sample for the presence of an ion channel gene nucleic acid, comprising:

a) contacting said sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said ion channel gene nucleic acid under conditions appropriate for hybridization, and

b) assessing whether hybridization has occurred between an ion channel gene nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said ion channel gene nucleic acid;

where if hybridization has occurred, an ion channel gene is present in the nucleic acid.

42. The method of Claim 41, wherein said nucleic acid comprising a contiguous nucleotide sequence is completely complementary to a part of the sequence of said ion channel gene nucleic acid.

43. The method of Claim 41, comprising amplification of at least part of said ion channel gene nucleic acid.

44. The method of Claim 41, wherein said contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table I; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table I; or c) capable of selectively hybridizing to said ion channel gene nucleic acid.

45. A reagent for assaying a sample for the presence of an ion channel gene nucleic acid, said reagent comprising a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said ion channel gene nucleic acid.

46. The reagent of Claim 45, wherein the nucleic acid comprises a contiguous nucleotide sequence which is completely complementary to a part of the nucleotide sequence of said ion channel gene nucleic acid.

47. A reagent kit for assaying a sample for the presence of an ion channel gene nucleic acid, comprising in separate containers:

a) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said ion channel gene nucleic acid, and

b) reagents for detection of said label.

48. The reagent kit of Claim 47, wherein the labeled nucleic acid comprises a contiguous nucleotide sequences which is completely complementary to a part of the nucleotide sequence of said ion channel gene nucleic acid.

49. A reagent kit for assaying a sample for the presence of an ion channel gene nucleic acid, comprising one or more nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said ion channel gene nucleic acid, and which is capable of acting as a primer for said ion channel gene nucleic acid when maintained under conditions for primer extension.

50. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table I; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table I; or c) capable of selectively hybridizing to said ion channel gene nucleic acid, for assaying a sample for the presence of an ion channel gene nucleic acid.

51. The use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either:

a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table I;

b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table I; or

c) capable of selectively hybridizing to said ion channel gene nucleic acid;

for assaying a sample for the presence of an ion channel gene nucleic acid that has at least one nucleotide difference from the first nucleic acid.

52. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either:

a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table I;

b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table I; or

c) capable of selectively hybridizing to said ion channel gene nucleic acid;

for diagnosing a susceptibility to a disease or condition associated with an ion channel.

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Martinez, Roger Alfonso Moraga
Sigurdsson, Gunnar Thor

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ctc tac cga gtg cac atg ggc cgc aag cct ggc tac ttc tcc ttc ctg   1632
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ccc ctt gca aca gtg ggg agc aga tcc aaa aca gca tct ccc tcg agt   288
Pro Leu Ala Thr Val Gly Ser Arg Ser Lys Thr Ala Ser Pro Ser Ser
                85                  90                  95

ctc tct ctt gct gcc tgc ttg att ttt cat cac agc act tgt cac tac   336
Leu Ser Leu Ala Ala Cys Leu Ile Phe His His Ser Thr Cys His Tyr
            100                 105                 110

ctg aca cag agt ctc ata agg gga aca ggc atg gca cat agt ctt att   384
Leu Thr Gln Ser Leu Ile Arg Gly Thr Gly Met Ala His Ser Leu Ile
        115                 120                 125

gag gtg ata ggt gta gtt agg gcc tca ttg ggt cgg gtg agg cat ttg   432
Glu Val Ile Gly Val Val Arg Ala Ser Leu Gly Arg Val Arg His Leu
    130                 135                 140

gat gac agt tta aga aca agg tgg ctg ggt gca gtg gct cat gct gag   480
Asp Asp Ser Leu Arg Thr Arg Trp Leu Gly Ala Val Ala His Ala Glu
145                 150                 155                 160

gca ggc gga tta cct gag gtc agg agt tcg aga tta acc tgg cca acg   528
Ala Gly Gly Leu Pro Glu Val Arg Ser Ser Arg Leu Thr Trp Pro Thr
                165                 170                 175

tgg cgc ctc agg cgt agc cag aaa gaa gct ggc acg aga gag agg ggt   576
Trp Arg Leu Arg Arg Ser Gln Lys Glu Ala Gly Thr Arg Glu Arg Gly
            180                 185                 190
```

```
ggc gag tgg ccc agg aat gcg gtg ggg gag ccg tcg gct gcc tgg aat   624
Gly Glu Trp Pro Arg Asn Ala Val Gly Glu Pro Ser Ala Ala Trp Asn
        195                 200                 205

gcc agg tcc gat ttc agg ccc aag gtg ggc tcc tgg agt cag tcc atg   672
Ala Arg Ser Asp Phe Arg Pro Lys Val Gly Ser Trp Ser Gln Ser Met
    210                 215                 220

ctc ctg gcc cct ccc cct ccc tac ctc tct ctc tct cgc ctc cct cag   720
Leu Leu Ala Pro Pro Pro Pro Tyr Leu Ser Leu Ser Arg Leu Pro Gln
225                 230                 235                 240

ttg ctc act ctc cgt gca ttt ctc tct aac tgt cca ctt ctg tct tcc   768
Leu Leu Thr Leu Arg Ala Phe Leu Ser Asn Cys Pro Leu Leu Ser Ser
                245                 250                 255

cct ctg tcc ccc tcc acc cct gcc cgg ctt ccc ctc cag cag aag gca   816
Pro Leu Ser Pro Ser Thr Pro Ala Arg Leu Pro Leu Gln Gln Lys Ala
            260                 265                 270

gac ctg gct gtg gcc gcc ttc acc atc aca gct gag cgg gag aag gtc   864
Asp Leu Ala Val Ala Ala Phe Thr Ile Thr Ala Glu Arg Glu Lys Val
        275                 280                 285

atc gac ttt tcc aag ccc ttt atg acc ctg ggg atc agc atc ctc tac   912
Ile Asp Phe Ser Lys Pro Phe Met Thr Leu Gly Ile Ser Ile Leu Tyr
    290                 295                 300

cga gtg cac atg ggc cgc aag cct ggc tac ttc tcc ttc ctg gac ccc   960
Arg Val His Met Gly Arg Lys Pro Gly Tyr Phe Ser Phe Leu Asp Pro
305                 310                 315                 320

ttc tcc cct gct gtg tgg ctc ttc atg ctt ctt gcc tac ctg gct gtc  1008
Phe Ser Pro Ala Val Trp Leu Phe Met Leu Leu Ala Tyr Leu Ala Val
                325                 330                 335

agc tgc gtc ctg ttt ctg gct gcc agg ctg agc ccc tat gag tgg tat  1056
Ser Cys Val Leu Phe Leu Ala Ala Arg Leu Ser Pro Tyr Glu Trp Tyr
            340                 345                 350

aac cca cac cca tgc ctg cgg gca cgc ccc cac atc ctg gag aac cag  1104
Asn Pro His Pro Cys Leu Arg Ala Arg Pro His Ile Leu Glu Asn Gln
        355                 360                 365

tac acg ctg ggc aac agc ctg tgg ttt ccc gtg ggg ggc ttc atg cag  1152
Tyr Thr Leu Gly Asn Ser Leu Trp Phe Pro Val Gly Gly Phe Met Gln
    370                 375                 380

cag ggc tcg gag atc atg ccc cgg gcg ctg tcc acg cgc tgt gtc agc  1200
Gln Gly Ser Glu Ile Met Pro Arg Ala Leu Ser Thr Arg Cys Val Ser
385                 390                 395                 400

gga gtc tgg tgg gcc ttc acc ttg atc atc atc tcc tcc tac acg gcc  1248
Gly Val Trp Trp Ala Phe Thr Leu Ile Ile Ile Ser Ser Tyr Thr Ala
                405                 410                 415

aac ctg gcc gcc ttc ctc acc gtg cag cgc atg gag gtg cct gtg gag  1296
Asn Leu Ala Ala Phe Leu Thr Val Gln Arg Met Glu Val Pro Val Glu
            420                 425                 430

tcg gcc gat gac ctg gca gat cag acc aac atc gag tat ggc acc atc  1344
Ser Ala Asp Asp Leu Ala Asp Gln Thr Asn Ile Glu Tyr Gly Thr Ile
        435                 440                 445
```

```
cac gcc ggc tcc acc atg acc ttc ttc cag aat tca cgg tac caa acg   1392
His Ala Gly Ser Thr Met Thr Phe Phe Gln Asn Ser Arg Tyr Gln Thr
    450                 455                 460

tac cag cgc atg tgg aac tac atg cag tcg aag cag ccc agc gtg ttc   1440
Tyr Gln Arg Met Trp Asn Tyr Met Gln Ser Lys Gln Pro Ser Val Phe
465                 470                 475                 480

gtc aag agc aca gaa gag ggc att gcc cgc gtc ctc aac tcc cgc tac   1488
Val Lys Ser Thr Glu Glu Gly Ile Ala Arg Val Leu Asn Ser Arg Tyr
                485                 490                 495

gcc ttc ctg ctc gag tcc acc atg aac gaa tac cac cgg cgc ctc aac   1536
Ala Phe Leu Leu Glu Ser Thr Met Asn Glu Tyr His Arg Arg Leu Asn
            500                 505                 510

tgc aac ctc acc cag atc ggg gga ctc ctc gac acc aag ggc tac ggc   1584
Cys Asn Leu Thr Gln Ile Gly Gly Leu Leu Asp Thr Lys Gly Tyr Gly
        515                 520                 525

att ggc atg ccg ctg ggc tcc ccg ttc cgg gat gag atc aca ctg gcc   1632
Ile Gly Met Pro Leu Gly Ser Pro Phe Arg Asp Glu Ile Thr Leu Ala
    530                 535                 540

atc ctg cag ctt cag gag aac aac cgg ctg gag atc ctg aag cgc aag   1680
Ile Leu Gln Leu Gln Glu Asn Asn Arg Leu Glu Ile Leu Lys Arg Lys
545                 550                 555                 560

tgg tgg gag ggg ggc cgg tgc ccc aag gag gag gac cat cga gct aaa   1728
Trp Trp Glu Gly Gly Arg Cys Pro Lys Glu Glu Asp His Arg Ala Lys
                565                 570                 575

ggt ttg ggc atg gag aac att ggt ggc att ttt atc gtg ctc atc tgt   1776
Gly Leu Gly Met Glu Asn Ile Gly Gly Ile Phe Ile Val Leu Ile Cys
            580                 585                 590

ggc ctc atc att gct gtc ttc gtg gcg gtc atg gaa ttc ata tgg tcc   1824
Gly Leu Ile Ile Ala Val Phe Val Ala Val Met Glu Phe Ile Trp Ser
        595                 600                 605

aca cgg agg tca gct gag tcc gag gag gtg tcg gtg tgc cag gag atg   1872
Thr Arg Arg Ser Ala Glu Ser Glu Glu Val Ser Val Cys Gln Glu Met
    610                 615                 620

ctg cag gag ctg cgc cac gcc gtt tct tgc cgc aag acg tcg cgt tcc   1920
Leu Gln Glu Leu Arg His Ala Val Ser Cys Arg Lys Thr Ser Arg Ser
625                 630                 635                 640

cgc cgg cgc cga cgc ccg ggc ggc ccg agc cgg gcc ctg ctg tca ctg   1968
Arg Arg Arg Arg Arg Pro Gly Gly Pro Ser Arg Ala Leu Leu Ser Leu
                645                 650                 655

cgc gcg gtc cgc gag atg cgc ctc agc aac ggc aag ctc tac tcg gcc   2016
Arg Ala Val Arg Glu Met Arg Leu Ser Asn Gly Lys Leu Tyr Ser Ala
            660                 665                 670

ggc gcg ggc ggg gat gcg ggc agc gcg cac ggg ggc ccg cag cgc ctc   2064
Gly Ala Gly Gly Asp Ala Gly Ser Ala His Gly Gly Pro Gln Arg Leu
        675                 680                 685

ctg gac gac ccg ggg ccc ccc agc gga gcc cga ccc gcc gcc ccc acc   2112
Leu Asp Asp Pro Gly Pro Pro Ser Gly Ala Arg Pro Ala Ala Pro Thr
```

690 695 700

ccc tgc acc cac gtg cgc gtc 2133
Pro Cys Thr His Val Arg Val
705 710

<210> 4
<211> 711
<212> PRT
<213> Homo sapiens

<400> 4
Met Leu Ala Arg Leu Val Ser Asn Thr Tyr Ala Gln Leu Ile Leu Lys
1 5 10 15
Ser Phe Cys Ser Ser Gln Ala Arg Trp Leu Thr Pro Val Ile Pro Ala
20 25 30
Leu Trp Glu Ala Glu Glu Gly Gly Ser Arg Gly Gln Glu Ile Glu Thr
35 40 45
Ile Leu Ala Asn Met Val Lys Arg Pro Trp Asn Leu Pro Pro Arg Ser
50 55 60
Ser Pro Ala Phe Ser Val Leu Pro Ser Cys Cys Tyr Ser Asn Lys Thr
65 70 75 80
Pro Leu Ala Thr Val Gly Ser Arg Ser Lys Thr Ala Ser Pro Ser Ser
85 90 95
Leu Ser Leu Ala Ala Cys Leu Ile Phe His His Ser Thr Cys His Tyr
100 105 110
Leu Thr Gln Ser Leu Ile Arg Gly Thr Gly Met Ala His Ser Leu Ile
115 120 125
Glu Val Ile Gly Val Val Arg Ala Ser Leu Gly Arg Val Arg His Leu
130 135 140
Asp Asp Ser Leu Arg Thr Arg Trp Leu Gly Ala Val Ala His Ala Glu
145 150 155 160
Ala Gly Gly Leu Pro Glu Val Arg Ser Ser Arg Leu Thr Trp Pro Thr
165 170 175
Trp Arg Leu Arg Arg Ser Gln Lys Glu Ala Gly Thr Arg Glu Arg Gly
180 185 190
Gly Glu Trp Pro Arg Asn Ala Val Gly Glu Pro Ser Ala Ala Trp Asn
195 200 205
Ala Arg Ser Asp Phe Arg Pro Lys Val Gly Ser Trp Ser Gln Ser Met
210 215 220
Leu Leu Ala Pro Pro Pro Pro Tyr Leu Ser Leu Ser Arg Leu Pro Gln
225 230 235 240
Leu Leu Thr Leu Arg Ala Phe Leu Ser Asn Cys Pro Leu Leu Ser Ser
245 250 255
Pro Leu Ser Pro Ser Thr Pro Ala Arg Leu Pro Leu Gln Gln Lys Ala
260 265 270
Asp Leu Ala Val Ala Ala Phe Thr Ile Thr Ala Glu Arg Glu Lys Val
275 280 285
Ile Asp Phe Ser Lys Pro Phe Met Thr Leu Gly Ile Ser Ile Leu Tyr
290 295 300
Arg Val His Met Gly Arg Lys Pro Gly Tyr Phe Ser Phe Leu Asp Pro
305 310 315 320
Phe Ser Pro Ala Val Trp Leu Phe Met Leu Leu Ala Tyr Leu Ala Val
325 330 335
Ser Cys Val Leu Phe Leu Ala Ala Arg Leu Ser Pro Tyr Glu Trp Tyr
340 345 350
Asn Pro His Pro Cys Leu Arg Ala Arg Pro His Ile Leu Glu Asn Gln
355 360 365
Tyr Thr Leu Gly Asn Ser Leu Trp Phe Pro Val Gly Gly Phe Met Gln
370 375 380
Gln Gly Ser Glu Ile Met Pro Arg Ala Leu Ser Thr Arg Cys Val Ser
385 390 395 400

```
Gly Val Trp Trp Ala Phe Thr Leu Ile Ile Ile Ser Ser Tyr Thr Ala
                405                 410                 415
Asn Leu Ala Ala Phe Leu Thr Val Gln Arg Met Glu Val Pro Val Glu
            420                 425                 430
Ser Ala Asp Asp Leu Ala Asp Gln Thr Asn Ile Glu Tyr Gly Thr Ile
        435                 440                 445
His Ala Gly Ser Thr Met Thr Phe Phe Gln Asn Ser Arg Tyr Gln Thr
    450                 455                 460
Tyr Gln Arg Met Trp Asn Tyr Met Gln Ser Lys Gln Pro Ser Val Phe
465                 470                 475                 480
Val Lys Ser Thr Glu Glu Gly Ile Ala Arg Val Leu Asn Ser Arg Tyr
                485                 490                 495
Ala Phe Leu Leu Glu Ser Thr Met Asn Glu Tyr His Arg Arg Leu Asn
            500                 505                 510
Cys Asn Leu Thr Gln Ile Gly Gly Leu Leu Asp Thr Lys Gly Tyr Gly
        515                 520                 525
Ile Gly Met Pro Leu Gly Ser Pro Phe Arg Asp Glu Ile Thr Leu Ala
    530                 535                 540
Ile Leu Gln Leu Gln Glu Asn Asn Arg Leu Glu Ile Leu Lys Arg Lys
545                 550                 555                 560
Trp Trp Glu Gly Gly Arg Cys Pro Lys Glu Glu Asp His Arg Ala Lys
                565                 570                 575
Gly Leu Gly Met Glu Asn Ile Gly Gly Ile Phe Ile Val Leu Ile Cys
            580                 585                 590
Gly Leu Ile Ile Ala Val Phe Val Ala Val Met Glu Phe Ile Trp Ser
        595                 600                 605
Thr Arg Arg Ser Ala Glu Ser Glu Glu Val Ser Val Cys Gln Glu Met
    610                 615                 620
Leu Gln Glu Leu Arg His Ala Val Ser Cys Arg Lys Thr Ser Arg Ser
625                 630                 635                 640
Arg Arg Arg Arg Arg Pro Gly Gly Pro Ser Arg Ala Leu Leu Ser Leu
                645                 650                 655
Arg Ala Val Arg Glu Met Arg Leu Ser Asn Gly Lys Leu Tyr Ser Ala
            660                 665                 670
Gly Ala Gly Gly Asp Ala Gly Ser Ala His Gly Gly Pro Gln Arg Leu
        675                 680                 685
Leu Asp Asp Pro Gly Pro Pro Ser Gly Ala Arg Pro Ala Ala Pro Thr
    690                 695                 700
Pro Cys Thr His Val Arg Val
705                 710
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<210> 5
<211> 1356
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1356)

<400> 5

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ttt ttg atg tac tgt tgg gtt cag ttt gcc tta ttt att ttg agg gtt   48
Phe Leu Met Tyr Cys Trp Val Gln Phe Ala Leu Phe Ile Leu Arg Val
 1               5                  10                  15

ttt gca tct att gtt gat aag gca gat gat gaa gat gat gag gat tta   96
Phe Ala Ser Ile Val Asp Lys Ala Asp Asp Glu Asp Asp Glu Asp Leu
            20                  25                  30

acg gtg aac aaa acc tgg gtc ttg gcc cca aaa att cat gaa gga gat   144
Thr Val Asn Lys Thr Trp Val Leu Ala Pro Lys Ile His Glu Gly Asp
        35                  40                  45
```

```
atc aca caa att ctg aat tca ttg ctt caa ggc tat gac aat aaa ctt   192
Ile Thr Gln Ile Leu Asn Ser Leu Leu Gln Gly Tyr Asp Asn Lys Leu
     50                  55                  60

cgt cca gat ata gga gtg agg ccc aca gta att gaa act gat gtt tat   240
Arg Pro Asp Ile Gly Val Arg Pro Thr Val Ile Glu Thr Asp Val Tyr
 65                  70                  75                  80

gta aac agc att gga cca gtt gat cca att aat atg gaa tat aca ata   288
Val Asn Ser Ile Gly Pro Val Asp Pro Ile Asn Met Glu Tyr Thr Ile
                 85                  90                  95

gat ata att ttt gcc caa acc tgg ttt gac agt cgt tta aaa ttc aat   336
Asp Ile Ile Phe Ala Gln Thr Trp Phe Asp Ser Arg Leu Lys Phe Asn
            100                 105                 110

agt acc atg aaa gtg ctt atg ctt aac agt aat atg gtt gga aaa att   384
Ser Thr Met Lys Val Leu Met Leu Asn Ser Asn Met Val Gly Lys Ile
        115                 120                 125

tgg att cct gac act ttc ttc aga aac tca aga aaa tct gat gct cac   432
Trp Ile Pro Asp Thr Phe Phe Arg Asn Ser Arg Lys Ser Asp Ala His
    130                 135                 140

tgg ata aca act cct aat cgt ctg ctt cga att tgg aat gat gga cga   480
Trp Ile Thr Thr Pro Asn Arg Leu Leu Arg Ile Trp Asn Asp Gly Arg
145                 150                 155                 160

gtt ctg tat act cta aga ttg aca att aat gca gaa tgt tat ctt cag   528
Val Leu Tyr Thr Leu Arg Leu Thr Ile Asn Ala Glu Cys Tyr Leu Gln
                165                 170                 175

ctt cat aac ttt ccc atg gat gaa cat tcc tgt cca ctg gaa ttt tca   576
Leu His Asn Phe Pro Met Asp Glu His Ser Cys Pro Leu Glu Phe Ser
            180                 185                 190

agc tat gga tac cct aaa aat gaa att gaa tta tat cag ttt gca ttt   624
Ser Tyr Gly Tyr Pro Lys Asn Glu Ile Glu Leu Tyr Gln Phe Ala Phe
        195                 200                 205

gta ggg tta cgg aac tca act gaa atc act cac acg atc tct ggg gat   672
Val Gly Leu Arg Asn Ser Thr Glu Ile Thr His Thr Ile Ser Gly Asp
    210                 215                 220

tat gtt atc atg aca att ttt ttt gac ctg agc aga aga atg gga tat   720
Tyr Val Ile Met Thr Ile Phe Phe Asp Leu Ser Arg Arg Met Gly Tyr
225                 230                 235                 240

ttc act att cag acc tac att cca tgc att ctg aca gtt gtt ctt tct   768
Phe Thr Ile Gln Thr Tyr Ile Pro Cys Ile Leu Thr Val Val Leu Ser
                245                 250                 255

tgg gtg tct ttt tgg atc aat aaa gat gca gtg cct gca aga aca tcg   816
Trp Val Ser Phe Trp Ile Asn Lys Asp Ala Val Pro Ala Arg Thr Ser
            260                 265                 270

ttg ggt atc act aca gtt ctg act atg aca acc ctg agt aca att gcc   864
Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Leu Ser Thr Ile Ala
        275                 280                 285

agg aag tct tta cct aag gtt tct tat gtg act gcg atg gat ctc ttt   912
Arg Lys Ser Leu Pro Lys Val Ser Tyr Val Thr Ala Met Asp Leu Phe
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```
    290                 295                 300

gtt tct gtt tgt ttc att ttt gtt ttt gca gcc ttg atg gaa tat gga    960
Val Ser Val Cys Phe Ile Phe Val Phe Ala Ala Leu Met Glu Tyr Gly
305                 310                 315                 320

acc ttg cat tat ttt acc agc aac caa aaa gga aag act gct act aaa   1008
Thr Leu His Tyr Phe Thr Ser Asn Gln Lys Gly Lys Thr Ala Thr Lys
                325                 330                 335

gac aga aag cta aaa aat aaa gcc tcg gcc tca tca gga ata aac agt   1056
Asp Arg Lys Leu Lys Asn Lys Ala Ser Ala Ser Ser Gly Ile Asn Ser
            340                 345                 350

aac aat gac aac aat aat gat gtt acc tac tgg cag atg act cct ggt   1104
Asn Asn Asp Asn Asn Asn Asp Val Thr Tyr Trp Gln Met Thr Pro Gly
        355                 360                 365

ctc cat cct gga tcc act ctg att cca atg aat aat att tct gtg ccg   1152
Leu His Pro Gly Ser Thr Leu Ile Pro Met Asn Asn Ile Ser Val Pro
    370                 375                 380

caa gaa gat gat tat ggg tat cag tgt ttg gag ggc aaa gat tgt gcc   1200
Gln Glu Asp Asp Tyr Gly Tyr Gln Cys Leu Glu Gly Lys Asp Cys Ala
385                 390                 395                 400

agc ttc ttc tgt tgc ttt gaa gac tgc aga aca gga tct tgg agg gaa   1248
Ser Phe Phe Cys Cys Phe Glu Asp Cys Arg Thr Gly Ser Trp Arg Glu
                405                 410                 415

gga agg ata cac ata cgc att gcc aaa att gac tct tat tct aga ata   1296
Gly Arg Ile His Ile Arg Ile Ala Lys Ile Asp Ser Tyr Ser Arg Ile
            420                 425                 430

ttt ttc cca acc gct ttt gcc ctg ttc aac ttg gtt tat tgg gtt ggc   1344
Phe Phe Pro Thr Ala Phe Ala Leu Phe Asn Leu Val Tyr Trp Val Gly
        435                 440                 445

tat ctt tac tta                                                  1356
Tyr Leu Tyr Leu
    450
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<210> 6
<211> 452
<212> PRT
<213> Homo sapiens

<400> 6

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Phe Leu Met Tyr Cys Trp Val Gln Phe Ala Leu Phe Ile Leu Arg Val
 1               5                  10                  15
Phe Ala Ser Ile Val Asp Lys Ala Asp Asp Glu Asp Asp Glu Asp Leu
            20                  25                  30
Thr Val Asn Lys Thr Trp Val Leu Ala Pro Lys Ile His Glu Gly Asp
        35                  40                  45
Ile Thr Gln Ile Leu Asn Ser Leu Leu Gln Gly Tyr Asp Asn Lys Leu
    50                  55                  60
Arg Pro Asp Ile Gly Val Arg Pro Thr Val Ile Glu Thr Asp Val Tyr
65                  70                  75                  80
Val Asn Ser Ile Gly Pro Val Asp Pro Ile Asn Met Glu Tyr Thr Ile
                85                  90                  95
Asp Ile Ile Phe Ala Gln Thr Trp Phe Asp Ser Arg Leu Lys Phe Asn
            100                 105                 110
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```
Ser Thr Met Lys Val Leu Met Leu Asn Ser Asn Met Val Gly Lys Ile
        115                 120                 125
Trp Ile Pro Asp Thr Phe Phe Arg Asn Ser Arg Lys Ser Asp Ala His
    130                 135                 140
Trp Ile Thr Thr Pro Asn Arg Leu Leu Arg Ile Trp Asn Asp Gly Arg
145                 150                 155                 160
Val Leu Tyr Thr Leu Arg Leu Thr Ile Asn Ala Glu Cys Tyr Leu Gln
                165                 170                 175
Leu His Asn Phe Pro Met Asp Glu His Ser Cys Pro Leu Glu Phe Ser
            180                 185                 190
Ser Tyr Gly Tyr Pro Lys Asn Glu Ile Glu Leu Tyr Gln Phe Ala Phe
        195                 200                 205
Val Gly Leu Arg Asn Ser Thr Glu Ile Thr His Thr Ile Ser Gly Asp
    210                 215                 220
Tyr Val Ile Met Thr Ile Phe Phe Asp Leu Ser Arg Arg Met Gly Tyr
225                 230                 235                 240
Phe Thr Ile Gln Thr Tyr Ile Pro Cys Ile Leu Thr Val Val Leu Ser
                245                 250                 255
Trp Val Ser Phe Trp Ile Asn Lys Asp Ala Val Pro Ala Arg Thr Ser
            260                 265                 270
Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Leu Ser Thr Ile Ala
        275                 280                 285
Arg Lys Ser Leu Pro Lys Val Ser Tyr Val Thr Ala Met Asp Leu Phe
    290                 295                 300
Val Ser Val Cys Phe Ile Phe Val Phe Ala Ala Leu Met Glu Tyr Gly
305                 310                 315                 320
Thr Leu His Tyr Phe Thr Ser Asn Gln Lys Gly Lys Thr Ala Thr Lys
                325                 330                 335
Asp Arg Lys Leu Lys Asn Lys Ala Ser Ala Ser Ser Gly Ile Asn Ser
            340                 345                 350
Asn Asn Asp Asn Asn Asn Asp Val Thr Tyr Trp Gln Met Thr Pro Gly
        355                 360                 365
Leu His Pro Gly Ser Thr Leu Ile Pro Met Asn Asn Ile Ser Val Pro
    370                 375                 380
Gln Glu Asp Asp Tyr Gly Tyr Gln Cys Leu Glu Gly Lys Asp Cys Ala
385                 390                 395                 400
Ser Phe Phe Cys Cys Phe Glu Asp Cys Arg Thr Gly Ser Trp Arg Glu
                405                 410                 415
Gly Arg Ile His Ile Arg Ile Ala Lys Ile Asp Ser Tyr Ser Arg Ile
            420                 425                 430
Phe Phe Pro Thr Ala Phe Ala Leu Phe Asn Leu Val Tyr Trp Val Gly
        435                 440                 445
Tyr Leu Tyr Leu
    450
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<210> 7
<211> 1479
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1479)

<221> misc_feature
<222> (1)...(1479)
<223> n = A,T,C or G

<400> 7

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ctg agt tat cac tat tgg act tgg gct ttt ctc agt gaa aac aac tct   48
Leu Ser Tyr His Tyr Trp Thr Trp Ala Phe Leu Ser Glu Asn Asn Ser
 1               5                  10                  15
```

```
cca aaa gtc cag agt tta aga aga ggg gtt agt cga ttg tcc cgt atc   96
Pro Lys Val Gln Ser Leu Arg Arg Gly Val Ser Arg Leu Ser Arg Ile
            20                  25                  30

cta tta ctt ccg atc cat tct ctc atg ggt cat gac ctc agc ctg gag  144
Leu Leu Leu Pro Ile His Ser Leu Met Gly His Asp Leu Ser Leu Glu
        35                  40                  45

atg acc gga gtc tca cta gca gtt tta ctg gag tct att gat cct ctt  192
Met Thr Gly Val Ser Leu Ala Val Leu Leu Glu Ser Ile Asp Pro Leu
    50                  55                  60

tca gag aat gac ttt aca atg act ttt tat ctc agg cat tac tgg aaa  240
Ser Glu Asn Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
65                  70                  75                  80

gac gag agg ctc tcc ttt cct agc aca gca aac aaa agc atg aca ttt  288
Asp Glu Arg Leu Ser Phe Pro Ser Thr Ala Asn Lys Ser Met Thr Phe
                85                  90                  95

gat cat aga ttg acc aga aag atc tgg gtg cct gat atc ttt ttt gtc  336
Asp His Arg Leu Thr Arg Lys Ile Trp Val Pro Asp Ile Phe Phe Val
            100                 105                 110

cac tct aaa aga tcc ttc atc cat gat aca act atg gag aat atc atg  384
His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Met Glu Asn Ile Met
        115                 120                 125

ctg cgc gta cac cct gat gga aac gtc ctc cta agt ctc agg ata acg  432
Leu Arg Val His Pro Asp Gly Asn Val Leu Leu Ser Leu Arg Ile Thr
    130                 135                 140

gtt tcg gcc atg tgc ttt atg gat ttc agc agg ttt cct ctt gac act  480
Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
145                 150                 155                 160

caa aat tgt tct ctt gaa ctg gaa agc tat gcc tac aat gag gat gac  528
Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn Glu Asp Asp
                165                 170                 175

cta atg cta tac tgg aaa cac gga aac aag tcc tta aat act gaa gaa  576
Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu
            180                 185                 190

cat atg tcc ctt tct cag ttc ttc att gaa gac ttc agt gca tct agt  624
His Met Ser Leu Ser Gln Phe Phe Ile Glu Asp Phe Ser Ala Ser Ser
        195                 200                 205

gga tta gct ttc tat agc agc aca ggt tgg tac aat agg ctt ttc atc  672
Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Asn Arg Leu Phe Ile
    210                 215                 220

aac ttt gtg cta agg agg cat gtt ttc ttc ttt gtg ctg caa acc tat  720
Asn Phe Val Leu Arg Arg His Val Phe Phe Phe Val Leu Gln Thr Tyr
225                 230                 235                 240

ttc cca gcc ata ttg atg gtg atg ctt tca tgg gtt tca ttt tgg att  768
Phe Pro Ala Ile Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
                245                 250                 255

gac cga aga gct gtt cct gca aga gtt tcc ctg gga atc acc aca gtg  816
Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
```

```
            260                 265                 270

ctg acc atg tcc aca atc atc act gct gtg agc gcc tcc atg ccc cag   864
Leu Thr Met Ser Thr Ile Ile Thr Ala Val Ser Ala Ser Met Pro Gln
        275                 280                 285

gtg tcc tac ctc aag gct gtg gat gtg tac ctg tgg gtc agc tcc ctc   912
Val Ser Tyr Leu Lys Ala Val Asp Val Tyr Leu Trp Val Ser Ser Leu
    290                 295                 300

ttt gtg ttc ctg tca gtc att gag tat gca gct gtg aac tac ctc acc   960
Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
305                 310                 315                 320

aca aat aag act ccg tct aaa aaa aaa aaa aga aga agt ctt gat ggc   1008
Thr Asn Lys Thr Pro Ser Lys Lys Lys Lys Arg Arg Ser Leu Asp Gly
                325                 330                 335

aaa cca aat cca cca cat ccc agc ttc gtg ttc cag gtt aag tct cct   1056
Lys Pro Asn Pro Pro His Pro Ser Phe Val Phe Gln Val Lys Ser Pro
            340                 345                 350

aaa ccc ctt ctg tgt ttc cac agt ggt gtc att tct tcc cca tgg cac   1104
Lys Pro Leu Leu Cys Phe His Ser Gly Val Ile Ser Ser Pro Trp His
        355                 360                 365

ttg aag cta ctt caa gcc cca tcc ggg ctg gaa ctg gtg tcg ggg gag   1152
Leu Lys Leu Leu Gln Ala Pro Ser Gly Leu Glu Leu Val Ser Gly Glu
    370                 375                 380

cca tgg atg aat cgt atg ccc tgg tgt tgg atg tac aat att gat gca   1200
Pro Trp Met Asn Arg Met Pro Trp Cys Trp Met Tyr Asn Ile Asp Ala
385                 390                 395                 400

gtt caa gct atg gcc ttt gat ggt tgt tac cat gac agc gag att gac   1248
Val Gln Ala Met Ala Phe Asp Gly Cys Tyr His Asp Ser Glu Ile Asp
                405                 410                 415

atg gac cag act tcc ctc tct cta aac tca gaa gac ttc atg aga aga   1296
Met Asp Gln Thr Ser Leu Ser Leu Asn Ser Glu Asp Phe Met Arg Arg
            420                 425                 430

aaa tcg ata tgc agc ccc agc acc gat tca tct cgg ata aag aga aga   1344
Lys Ser Ile Cys Ser Pro Ser Thr Asp Ser Ser Arg Ile Lys Arg Arg
        435                 440                 445

aaa tcc cta gga gga cat gtt ggt aga atc att ctg gaa aac aac cat   1392
Lys Ser Leu Gly Gly His Val Gly Arg Ile Ile Leu Glu Asn Asn His
    450                 455                 460

gtc att gac acc tat tct agg att ttn tat tcc cca ttg tgt ata tct   1440
Val Ile Asp Thr Tyr Ser Arg Ile Xaa Tyr Ser Pro Leu Cys Ile Ser
465                 470                 475                 480

tta ttt aat ttg ttt tac tgg ggt gta tat ctc aac cgt               1479
Leu Phe Asn Leu Phe Tyr Trp Gly Val Tyr Leu Asn Arg
                485                 490
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<210> 8
<211> 493
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(492)
<223> Xaa = Any Amino Acid

<400> 8

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Leu Ser Tyr His Tyr Trp Thr Trp Ala Phe Leu Ser Glu Asn Asn Ser
 1               5                  10                  15
Pro Lys Val Gln Ser Leu Arg Arg Gly Val Ser Arg Leu Ser Arg Ile
            20                  25                  30
Leu Leu Leu Pro Ile His Ser Leu Met Gly His Asp Leu Ser Leu Glu
        35                  40                  45
Met Thr Gly Val Ser Leu Ala Val Leu Leu Glu Ser Ile Asp Pro Leu
    50                  55                  60
Ser Glu Asn Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
65                  70                  75                  80
Asp Glu Arg Leu Ser Phe Pro Ser Thr Ala Asn Lys Ser Met Thr Phe
                85                  90                  95
Asp His Arg Leu Thr Arg Lys Ile Trp Val Pro Asp Ile Phe Phe Val
            100                 105                 110
His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Met Glu Asn Ile Met
        115                 120                 125
Leu Arg Val His Pro Asp Gly Asn Val Leu Leu Ser Leu Arg Ile Thr
    130                 135                 140
Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
145                 150                 155                 160
Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn Glu Asp Asp
                165                 170                 175
Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu
            180                 185                 190
His Met Ser Leu Ser Gln Phe Phe Ile Glu Asp Phe Ser Ala Ser Ser
        195                 200                 205
Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Asn Arg Leu Phe Ile
    210                 215                 220
Asn Phe Val Leu Arg Arg His Val Phe Phe Phe Val Leu Gln Thr Tyr
225                 230                 235                 240
Phe Pro Ala Ile Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
                245                 250                 255
Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
            260                 265                 270
Leu Thr Met Ser Thr Ile Ile Thr Ala Val Ser Ala Ser Met Pro Gln
        275                 280                 285
Val Ser Tyr Leu Lys Ala Val Asp Val Tyr Leu Trp Val Ser Ser Leu
    290                 295                 300
Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
305                 310                 315                 320
Thr Asn Lys Thr Pro Ser Lys Lys Lys Lys Arg Arg Ser Leu Asp Gly
                325                 330                 335
Lys Pro Asn Pro Pro His Pro Ser Phe Val Phe Gln Val Lys Ser Pro
            340                 345                 350
Lys Pro Leu Leu Cys Phe His Ser Gly Val Ile Ser Ser Pro Trp His
        355                 360                 365
Leu Lys Leu Leu Gln Ala Pro Ser Gly Leu Glu Leu Val Ser Gly Glu
    370                 375                 380
Pro Trp Met Asn Arg Met Pro Trp Cys Trp Met Tyr Asn Ile Asp Ala
385                 390                 395                 400
Val Gln Ala Met Ala Phe Asp Gly Cys Tyr His Asp Ser Glu Ile Asp
                405                 410                 415
Met Asp Gln Thr Ser Leu Ser Leu Asn Ser Glu Asp Phe Met Arg Arg
            420                 425                 430
Lys Ser Ile Cys Ser Pro Ser Thr Asp Ser Ser Arg Ile Lys Arg Arg
        435                 440                 445
Lys Ser Leu Gly Gly His Val Gly Arg Ile Ile Leu Glu Asn Asn His
```

```
    450                 455                 460
Val Ile Asp Thr Tyr Ser Arg Ile Xaa Tyr Ser Pro Leu Cys Ile Ser
465                 470                 475                 480
Leu Phe Asn Leu Phe Tyr Trp Gly Val Tyr Leu Asn Arg
                485                 490
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<210> 9
<211> 1065
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1065)

<400> 9

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ttc tat tta ctt act tat tca ttt att tta gag tta gta agt tcc ata   48
Phe Tyr Leu Leu Thr Tyr Ser Phe Ile Leu Glu Leu Val Ser Ser Ile
 1               5                  10                  15

tct ggt agt tcc cac cac cag aga gag act gac atg cat tta ttt gct   96
Ser Gly Ser Ser His His Gln Arg Glu Thr Asp Met His Leu Phe Ala
            20                  25                  30

ctc act ttg gca agt ctt ttg tta gat tta cgt ggc ttg gac tac aaa   144
Leu Thr Leu Ala Ser Leu Leu Leu Asp Leu Arg Gly Leu Asp Tyr Lys
        35                  40                  45

ctc ctt cat ggt ttg ggc tcc ctc cca gtc aag gaa aca gct ctt gcc   192
Leu Leu His Gly Leu Gly Ser Leu Pro Val Lys Glu Thr Ala Leu Ala
    50                  55                  60

cca ctt gtt tcc ttt tcc atg gtt agt agc agc aac atg caa gac caa   240
Pro Leu Val Ser Phe Ser Met Val Ser Ser Ser Asn Met Gln Asp Gln
65                  70                  75                  80

aga gac caa tac cat ctc cct gtc aat ctt tta att ctg gac atg gtg   288
Arg Asp Gln Tyr His Leu Pro Val Asn Leu Leu Ile Leu Asp Met Val
                85                  90                  95

gat ttc ggg cac tgg atg act gaa tcc agc agg cta aag ggt gat aat   336
Asp Phe Gly His Trp Met Thr Glu Ser Ser Arg Leu Lys Gly Asp Asn
            100                 105                 110

agc tca tca act cat ggc ctg tcg tgg aag aga tct gca tgt gat tat   384
Ser Ser Ser Thr His Gly Leu Ser Trp Lys Arg Ser Ala Cys Asp Tyr
        115                 120                 125

gtt gtc atg act ata tat ttt gaa ttg agt aga aga atg gga tac ttc   432
Val Val Met Thr Ile Tyr Phe Glu Leu Ser Arg Arg Met Gly Tyr Phe
    130                 135                 140

acc att cag aca tac att ccc tgt ata ctg act gtg gtt tta tcc tgg   480
Thr Ile Gln Thr Tyr Ile Pro Cys Ile Leu Thr Val Val Leu Ser Trp
145                 150                 155                 160

gtg tca ttt tgg atc aaa aaa gat gct acg cca gca aga aca gca tta   528
Val Ser Phe Trp Ile Lys Lys Asp Ala Thr Pro Ala Arg Thr Ala Leu
                165                 170                 175

ggc atc acc acg gtg ctg acc atg acc acc ctg agc acc atc gcc agg   576
Gly Ile Thr Thr Val Leu Thr Met Thr Thr Leu Ser Thr Ile Ala Arg
```

```
            180                 185                 190

aag tcc ttg cca cgc gtg tcc tac gtg acc gcc atg gac ctt ttt gtg   624
Lys Ser Leu Pro Arg Val Ser Tyr Val Thr Ala Met Asp Leu Phe Val
        195                 200                 205

acc gtg tgc ttc ctg ttt gtc ttc gcc gcg ctg atg gag tat gcc acc   672
Thr Val Cys Phe Leu Phe Val Phe Ala Ala Leu Met Glu Tyr Ala Thr
    210                 215                 220

ctc aac tac tat tcc agc tgt aga aaa cca acc acc acg aag aag aca   720
Leu Asn Tyr Tyr Ser Ser Cys Arg Lys Pro Thr Thr Thr Lys Lys Thr
225                 230                 235                 240

aca tcg tta cta cat cca gat tcc tca aga tgg att cct gag cga ata   768
Thr Ser Leu Leu His Pro Asp Ser Ser Arg Trp Ile Pro Glu Arg Ile
                245                 250                 255

agc cta caa gcc cct tcc aac tat tcc ctc ctg gac atg agg cca cca   816
Ser Leu Gln Ala Pro Ser Asn Tyr Ser Leu Leu Asp Met Arg Pro Pro
            260                 265                 270

cca act gcg atg atc act tta aac aat tcc gtt tac tgg cag gaa ttt   864
Pro Thr Ala Met Ile Thr Leu Asn Asn Ser Val Tyr Trp Gln Glu Phe
        275                 280                 285

gaa gat acc tgt gtc tat gag tgt ctg gat ggc aaa gac tgt cag agc   912
Glu Asp Thr Cys Val Tyr Glu Cys Leu Asp Gly Lys Asp Cys Gln Ser
    290                 295                 300

ttc ttc tgc tgc tat gaa gaa tgt aaa tca gga tcc tgg agg aaa ggg   960
Phe Phe Cys Cys Tyr Glu Glu Cys Lys Ser Gly Ser Trp Arg Lys Gly
305                 310                 315                 320

cgt att cac ata gac atc ttg gag ctg gac tcg tac tcc cgg gtc ttt  1008
Arg Ile His Ile Asp Ile Leu Glu Leu Asp Ser Tyr Ser Arg Val Phe
                325                 330                 335

ttc ccc acg tcc ttc ctg ctc ttt aac ctg gtc tac tgg gtt gga tac  1056
Phe Pro Thr Ser Phe Leu Leu Phe Asn Leu Val Tyr Trp Val Gly Tyr
            340                 345                 350

ctg tat ctc                                                     1065
Leu Tyr Leu
        355
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<210> 10
<211> 355
<212> PRT
<213> Homo sapiens

<400> 10

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Phe Tyr Leu Leu Thr Tyr Ser Phe Ile Leu Glu Leu Val Ser Ser Ile
 1               5                  10                  15
Ser Gly Ser Ser His His Gln Arg Glu Thr Asp Met His Leu Phe Ala
            20                  25                  30
Leu Thr Leu Ala Ser Leu Leu Leu Asp Leu Arg Gly Leu Asp Tyr Lys
        35                  40                  45
Leu Leu His Gly Leu Gly Ser Leu Pro Val Lys Glu Thr Ala Leu Ala
    50                  55                  60
Pro Leu Val Ser Phe Ser Met Val Ser Ser Ser Asn Met Gln Asp Gln
65                  70                  75                  80
```

```
Arg Asp Gln Tyr His Leu Pro Val Asn Leu Leu Ile Leu Asp Met Val
                85                  90                  95
Asp Phe Gly His Trp Met Thr Glu Ser Ser Arg Leu Lys Gly Asp Asn
            100                 105                 110
Ser Ser Ser Thr His Gly Leu Ser Trp Lys Arg Ser Ala Cys Asp Tyr
        115                 120                 125
Val Val Met Thr Ile Tyr Phe Glu Leu Ser Arg Arg Met Gly Tyr Phe
    130                 135                 140
Thr Ile Gln Thr Tyr Ile Pro Cys Ile Leu Thr Val Val Leu Ser Trp
145                 150                 155                 160
Val Ser Phe Trp Ile Lys Lys Asp Ala Thr Pro Ala Arg Thr Ala Leu
                165                 170                 175
Gly Ile Thr Thr Val Leu Thr Met Thr Thr Leu Ser Thr Ile Ala Arg
            180                 185                 190
Lys Ser Leu Pro Arg Val Ser Tyr Val Thr Ala Met Asp Leu Phe Val
        195                 200                 205
Thr Val Cys Phe Leu Phe Val Phe Ala Ala Leu Met Glu Tyr Ala Thr
    210                 215                 220
Leu Asn Tyr Tyr Ser Ser Cys Arg Lys Pro Thr Thr Thr Lys Lys Thr
225                 230                 235                 240
Thr Ser Leu Leu His Pro Asp Ser Ser Arg Trp Ile Pro Glu Arg Ile
                245                 250                 255
Ser Leu Gln Ala Pro Ser Asn Tyr Ser Leu Leu Asp Met Arg Pro Pro
            260                 265                 270
Pro Thr Ala Met Ile Thr Leu Asn Asn Ser Val Tyr Trp Gln Glu Phe
        275                 280                 285
Glu Asp Thr Cys Val Tyr Glu Cys Leu Asp Gly Lys Asp Cys Gln Ser
    290                 295                 300
Phe Phe Cys Cys Tyr Glu Glu Cys Lys Ser Gly Ser Trp Arg Lys Gly
305                 310                 315                 320
Arg Ile His Ile Asp Ile Leu Glu Leu Asp Ser Tyr Ser Arg Val Phe
                325                 330                 335
Phe Pro Thr Ser Phe Leu Leu Phe Asn Leu Val Tyr Trp Val Gly Tyr
            340                 345                 350
Leu Tyr Leu
        355
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